

REMARKS

Claims 12, 14-20 and 31-34 are amended. Claim 35 is added. Claims 22-30 have been withdrawn from consideration by the Examiner. Claims 12-14, 16-21 and 31-35 are active and under consideration.

At the outset, Applicants wish to thank Examiner Marvich for the helpful and courteous discussion conducted with their U.S. representative, on March 17, 2009. The supporting remarks for patentability are consistent with the remarks made during the discussion with the Examiner.

Claims 12-15, 19-21 and 31-34 stand rejected under 35 USC 102(b) as being anticipated by Poquet et al, J. Bacteriology, 1998, Vol. 180, pages 1904-1912.

However, this reference fails to disclose or suggest the claimed invention.

Notably, Poquet et al (J. Bacteriology, 1998, Vol. 180: 1904-1912) disclose a plasmid pFUN comprising sequence accession number GenBank U95834 which contains the sequence named nlp3 (see attached copy of NCBI description of GenBank U95834). The sequence accession number U95834 consists of:

- i) p_{Zn} promoter;
- ii) a sequence encoding ZitR; and
- iii) part of sequence coding for ZitS.

This sequence has been cloned in the polylinker of pFUN as to obtain expression of a fusion peptide n1p3/ΔNuc. Therefore, Poquet et al disclose a plasmid containing the p_{Zn} promoter (promoter sequence corresponding to SEQ ID NO: 1 of claimed expression cassette), a sequence encoding ZitR, the N-terminal part of ZitS fused with the sequence coding for ΔNuc, followed by the downstream restriction sites of the polylinker.

Amended claims 12 and 15 clearly relate to an expression cassette which does not contain

a sequence encoding any part of *L. lactis* ZitS. Consequently, the amended claims are clearly not anticipated by Poquet et al.

It is also clear that Poquet et al would have failed to have rendered the claimed invention obvious at the time it was made. Poquet et al identified among others a sequence (U95834 GenBank sequence) which contains n1p3 coding sequence. Poquet et al are only interested in exported peptide n1p3, and are totally silent about a possible function of the other nucleotide sequences contained in U95834 GenBank sequence. Nothing in the disclosure of Poquet et al or in accession number U95834 report would have suggested to the artisan that any other sequences contained in U95834 sequence could have a regulating function or code for a protein. See the attached NCBI description of GenBank U95834.

Therefore the person skilled in the art would not have been motivated to isolate specifically the nucleotide sequence corresponding to p_{Zn} promoter and sequence encoding ZitR from sequence GenBank accession number U95834 in order to engineer an expression cassette which has the characteristic to regulate expression of a gene according to the concentration of zinc in the culture medium.

Further, Poquet et al would not have enabled one skilled in the art to do so in any event.

Hence, this ground of rejection is unsustainable and should be withdrawn.

Claims 12-21 and 31-34 stand rejected under 35 USC 112, first paragraph, as the present specification ostensibly does not provide enablement for any embodiment of expression cassettes other than that containing SEQ ID NO: 1 operably linked to nucleotides 357-794 of SEQ ID NO: 2 further operably linked to a restriction site.

However, it is believed that the present claims are fully enabled by the present specification for the following reasons. The comments set forth below refer to Annex 1 and Annex 2, copies of

which are attached to this response.

First, the definition "at least 80% identity with the *Lactococcus lactis* ZitR protein GENBANK AAK06214" does not encompass a broad variety of proteins.

Second, Annex 1 shows the results of a BLAST search performed against the nr database which includes all the known protein sequences of all living organisms. Among these sequences, the only ones which share at least 80% identity with ZitR of *L. lactis* subsp. *Lactis* II1403 (GenBank AAK06214) are ZitR proteins, namely the ZitR protein of *L. lactis* subsp. *cremoris* MG1363 (88% identity) and the ZitR protein of *L. lactis* subsp. *cremoris* SK11 (89% identity). As a matter of fact there is no protein having at least 80% identity with GenBank AAK06214 which is not a ZitR protein. The next proteins which have the higher homology with ZitR are Streptococcus proteins which have at most 54% identity with GenBank AAK06214. Therefore, it is very unlikely that one can isolate a protein having 80% identity or more with GenBank AAK06214 which is not a ZitR protein.

Annex 2 shows the results of a BLAST search performed against the whole genome sequences of *L. lactis* subsp. *Lactis* II1403, *L. lactis* subsp. *cremoris* MG1363 and *L. lactis* subsp. *cremoris* SK11. There is no lactococcal protein, other than the ZitR proteins, having more than 38% identity with GenBank AAK06214.

Therefore using a probe derived from the sequence encoding GenBank AAK06214, or from nucleotides 357 to 794 of SEQ ID NO:9 of the instant application for screening a lactococcal DNA library, one of skill in the art would be able to easily discriminate a sequence encoding a ZitR protein from other lactococcal sequences.

Moreover, only the whole genome sequence of *L. lactis* subsp. *Lactis* II1403 (which was published in 2001) was available before the invention was made. The genome sequences of *Lactococcus lactis* subsp. *cremoris* SK11 and *Lactococcus lactis* subsp. *cremoris* MG1363 were only available in GenBank in 2006 and 2007 respectively. It is pointed out, however, that besides indicating GenBank AAK06214 as the reference sequence for a ZitR protein, the present application discloses another sequence encoding a ZitR protein, namely nucleotides 357 to 794 of SEQ ID NO:9, which encodes the ZitR protein of *lactis* subsp. *cremoris* MG1363.

Actually, the knowledge of the lactococcal genome sequences is not necessary to practice the claimed invention. As indicated above, one of ordinary skill in the art could have easily obtained polynucleotides encoding lactococcal ZitR proteins by screening a DNA library of a *Lactococcus* with a probe derived from the sequence encoding GenBank AAK06214, or from nucleotides 357 to 794 of SEQ ID NO:9.

BLAST results are provided herewith solely to evidence that the lactococcal genome does not contain any protein having more than 80% identity with GenBank AAK06214 which is not a ZitR protein.

Second, the two BLAST searches and results thereof noted above indicate that the present specification does in fact satisfy both the statutory enablement requirement under 35 USC 112, first paragraph, and the case law tests therefor cited by the Examiner.

Specifically, under the case law tests for enablement articulated in In re Wright and In re Fisher, cited by the Examiner, it is clear that since nucleotide sequences having more than 80% identity with GENBANK AAK06214 could easily be obtained by routine screening with a probe (as described above), undue experimentation would not be required.

Claims 12-16, 18-20 and 31-34 are objected to.

However, in view of the above claim amendments, this ground of rejection is deemed moot.

The specification stands objected to.

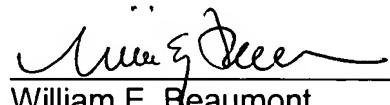
However, attached to this response is a Substitute Specification which meets the requirements of 37 CFR 1.77(b).

CONCLUSION

Accordingly, in view of all of the above, it is believed that this application is now in condition for allowance. Early notice to this effect is earnestly solicited.

Applicant hereby petitions for the Commissioner to charge any additional fees or any underpayment of fees which may be required to maintain the pendency of this case or credit any overpayment to Deposit Account No. 14-0112.

Respectfully submitted,
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NCBI description of
GenBank U95834

Nucleotide

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All Databases

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

Books

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for

Go Clear

Limits Preview/Index History Clipboard Details

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GenBank: U95834.1

Change Region Shown

Lactococcus lactis putative lipoprotein Nlp3 precursor, gene, partial cds

Customize View

Features Sequence

LOCUS LLU95834 945 bp DNA
linear BCT 24-APR-1998

DEFINITION Lactococcus lactis putative lipoprotein Nlp3 precursor, gene, partial cds.

ACCESSION U95834

VERSION U95834.1 GI:3043865

KEYWORDS .

SOURCE Lactococcus lactis subsp. cremoris MG1363

ORGANISM Lactococcus lactis subsp. cremoris MG1363

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.

REFERENCE 1 (bases 1 to 945)

AUTHORS Poquet, I., Ehrlich, S.D. and Gruss, A.

TITLE An export-specific reporter designed for gram-positive bacteria: application to Lactococcus lactis

JOURNAL J. Bacteriol. 180 (7), 1904-1912 (1998)

PUBMED 9537391

REFERENCE 2 (bases 1 to 945)

AUTHORS Poquet, I. and Gruss, A.

TITLE Direct Submission

JOURNAL Submitted (31-MAR-1997) Laboratoire de Génétique Appliquée-URLGA,
Institut National de la Recherche Agronomique,
CRJ, Jouy en Josas
78352, France

FEATURES Location/Qualifiers

source 1..945

/organism="Lactococcus lactis subsp.

cremoris MG1363"

/mol_type="genomic DNA"
/strain="MG1363"
/db_xref="taxon:416870"
complement(<1..330)
/note="identified as a fusion to a

CDS signal peptide-less form of the staphylococcal nuclease

reporter which displays nuclease activity; similar to

S. pneumoniae adhesion protein, Swiss-Prot Accession

Number P42363"

Pick Primers

Design and test primers for this sequence using Primer-BLAST.

Recent Activity

Turn Off Clear

Lactococcus lactis
putative lipoprotein

U95834 (1) Nucleotide

All links from this record

Full text in PMC

Protein

PubMed

Taxonomy

Related Sequences

```

/codon_start=1
/transl_table=11
/product="putative lipoprotein Nlp3"
precursor"
/protein_id="AAC14602.1"
/db_xref="GI:3043866"
/translation="MKKILMLFAIPAVLLLACQKTADKP
EVVTTFEPMYEFTKAIVG

DKVKIENIVPANQEVEFEPASKVATMTNAQAIYNSDDLEKWALKVNNKGVKIEAS
    KDVNKIKG"
    sig_peptide complement(277..330)
    /note="encodes lipoprotein-type signal
peptide"
    mat_peptide complement(<1..276)
    /product="putative lipoprotein Nlp3"
ORIGIN
    1 tccttaatt ttattgacat ctggcttgc ttctattttgc
actcccttat tattcacttt
    61 cagagcccat tttcaaggat catcagaatt ataaataata
gcttgagcat ttgtcattgt
    121 tgcaacttgc ttggcactcg gttcaaattc gtgaacttct
tgattcgccg gaacaatatt
    181 ttcaatttta accttatctc caacaatcgc ttctgtaaat
tcatacatcg gtcaaaaagt
    241 tgtcacaact tctggtttgt ctgctgtttt ttgacaacca
gcaagaagta aaactgccgg
    301 aatagcaaata aacatcaata ttttcttcat cgaaactcct
ccgtaagtac tgataagaat
    361 tgacttatca cttttggc ttctgtcagta aatttgcctc
ctaattcttgc ttaggtactt
    421 agattttctt catgtatggc agcatgttct ttagcaactg
gaatttgc ttctgtcagg
    481 ctccaaagga ctacgcgttc gtcattgtt gcccgacttg
attnaatcg ttcttgctct
    541 tgtaattttt tgagagctt agtaccgct gctggcgaaa
tcttgagttt ctcggcaatt
    601 ctgcgtttt tcgaaacccctc tgcaatcata atcattaaga
tatgttcttgc cgtgttgc
    661 agcttaacat tacttngca ttccggagtt aatatttcat
gcttggtttgc tccaaactgc
    721 ataattgccc caagaaactg gtcgatttga ttgtctaaan
tcatagtatt ttgtccctcca
    781 taatttagttt actggtaat tatatagcaa agtaaaaata
atgtcaacca gtaacatta
    841 ttttttactt ttttatttga aaaatcccttc catccttaag
ccgaacatca aaaaataaag
    901 ttttatttactt aacagtttga ccaccgctag ttgaaccagc tgaca
//
```

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BLAST Basic Local Alignment Search Tool

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gb|AAK06214| (145 letters)

Results for: **gb|AAK06214.1 zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis II1403](145aa)**
 Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|12725171|gb|AAK06214.1|AE006439_11

Description

zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis II1403]

Molecule type

amino acid

Query Length

145

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program

BLASTP 2.2.19+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#)

Search Parameters

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats	2
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date Mar 2, 2009 5:57 PM
 Number of letters 2,739,991,458
 Number of sequences 7,946,514
 Entrez query none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.310848	0.267
K	0.124161	0.041
H	0.32399	0.14

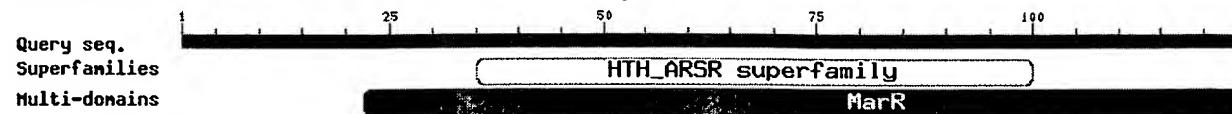
Results Statistics

Length adjustment 109
 Effective length of query 36
 Effective length of database 1873821432
 Effective search space 67457571552
 Effective search space used 67457571552

Graphic Summary

Show Conserved Domains

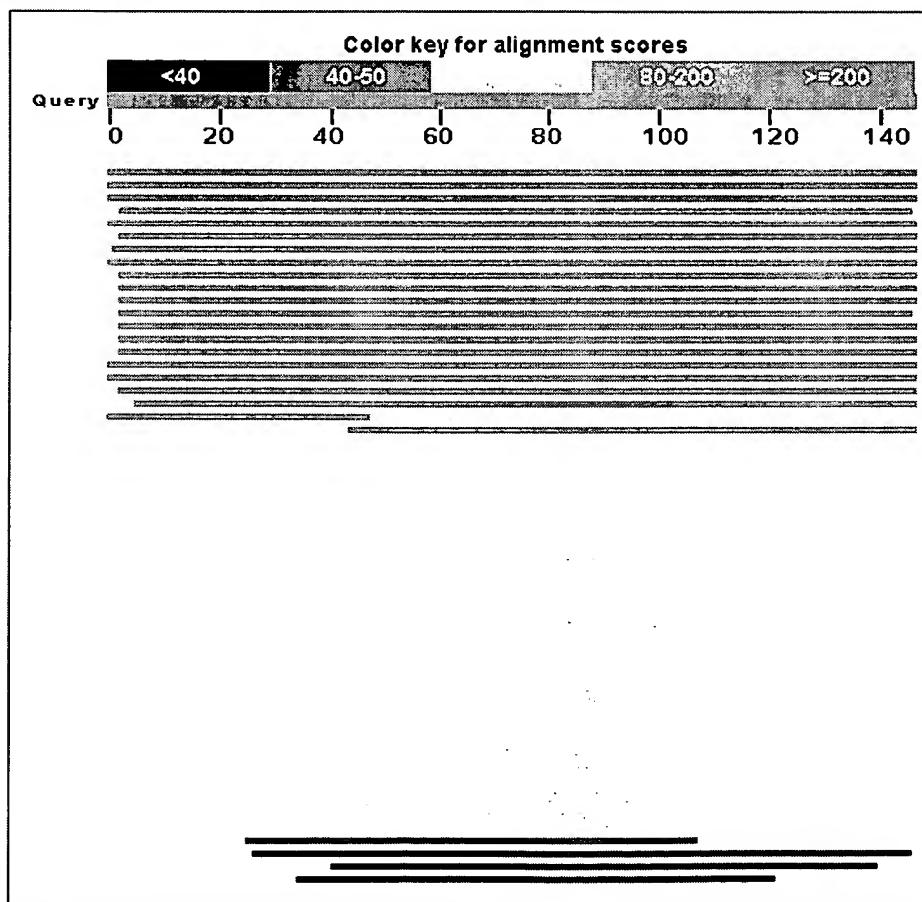
Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 100 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Descriptions

Sequences producing significant alignments:	Score (Bits)	E Value	G
ref NP_266273.1 zinc transport transcription regulator [Lactococcus lactis subsp. lactis] [MarR family]	291	1e-77	G
ref YP_511979.1 transcriptional regulator [Lactococcus lactis subsp. lactis] [MarR family]	268	1e-70	G
ref YP_001033643.1 transcriptional regulator of the zit operon [Lactococcus lactis subsp. lactis] [MarR family]	267	2e-70	G
ref YP_001034147.1 multiple antibiotic resistance operon transcriptional regulator [Lactococcus lactis subsp. lactis] [MarR family]	154	2e-36	G
ref NP_722293.1 putative transcriptional regulator [Streptococcus pneumoniae] [MarR family]	145	1e-33	G
ref YP_002122498.1 transcriptional repressor AdcR for Zn(2+)-responsive genes [Streptococcus pneumoniae] [MarR family]	143	3e-33	G
ref NP_606407.1 putative repressor protein [Streptococcus pneumoniae] [MarR family]	131	1e-32	G
ref ZP_02920004.1 hypothetical protein STRINF_00865 [Streptococcus pneumoniae] [MarR family]	141	2e-32	G
ref NP_268429.1 putative repressor protein [Streptococcus pneumoniae] [MarR family]	141	2e-32	G
ref YP_002561420.1 MarR-family regulatory protein [Streptococcus pneumoniae] [MarR family]	139	1e-31	G
ref NP_687190.1 adc operon repressor AdcR [Streptococcus agalactiae] [MarR family]	136	5e-31	G
ref YP_001451005.1 repressor protein adcR [Streptococcus gorilla] [MarR family]	133	4e-30	G
ref YP_01817760.1 adc operon repressor AdcR [Streptococcus pneumoniae] [MarR family]	132	6e-30	G
ref NP_582862.1 adc operon repressor AdcR [Streptococcus pneumoniae] [MarR family]	131	2e-29	G
ref NP_346556.1 adc operon repressor AdcR [Streptococcus pneumoniae] [MarR family]	130	2e-29	G
ref XP_138725.1 zinc transport transcriptional repressor [Streptococcus pneumoniae] [MarR family]	129	5e-29	G
ref YP_819746.1 zinc transport transcriptional repressor [Streptococcus pneumoniae] [MarR family]	128	1e-28	G
ref YP_001127479.1 transcriptional regulator [Streptococcus pneumoniae] [MarR family]	116	7e-25	G
ref ZP_03625066.1 transcriptional regulator, MarR family [Streptococcus pneumoniae] [MarR family]	110	4e-23	G
emb CRA75313.1 hypothetical protein [Lactococcus lactis subspecies lactis] [MarR family]	92.4	1e-17	G
ref ZP_00365496.1 COG1846: Transcriptional regulators [Streptococcus pneumoniae] [MarR family]	90.9	3e-17	G
ref YP_001485459.1 MarR family transcriptional regulator [Bacillus licheniformis ATCC 14580] >gb YP_001485459.1	67.0	5e-10	G
ref YP_001199372.1 transcriptional regulator [Streptococcus pneumoniae] [MarR family]	63.2	6e-09	G
ref YP_167316.1 MarR family transcriptional regulator [Staphylococcus aureus] [MarR family]	63.2	7e-09	G
ref YP_001777325.1 transcriptional repressor for Zn(2+)-responsive genes [Staphylococcus aureus] [MarR family]	62.8	8e-09	G
ref YP_501177.1 hypothetical protein SAOUHSC_02819 [Staphylococcus aureus] [MarR family]	62.8	8e-09	G
ref ZP_03583431.1 MarR family transcriptional regulator [Staphylococcus aureus] [MarR family]	61.2	3e-08	G
ref YP_174450.1 MarR family transcriptional regulator [Bacillus licheniformis ATCC 14580] >gb YP_174450.1	60.5	4e-08	G
ref YP_002661.1 transcriptional regulator YvnA [Bacillus licheniformis ATCC 14580] >gb YP_002661.1	59.3	1e-07	G
ref YP_254603.1 hypothetical protein pSHaeC05 [Staphylococcus aureus] [MarR family]	59.3	1e-07	G
ref YP_093087.1 YvnA [Bacillus licheniformis ATCC 14580] >gb YP_093087.1	59.3	1e-07	G
ref ZP_00728634.1 Transcriptional regulator, MarR family [Bacillus licheniformis ATCC 14580] >gb ZP_00728634.1	55.9	9e-07	G
ref ZP_02612091.1 transcriptional regulator, MarR family [Clostridium perfringens] >gb ZP_02612091.1	54.3	3e-06	G
ref YP_001253547.1 MarR family transcriptional regulator [Clostridium perfringens] >gb YP_001253547.1	54.3	3e-06	G
ref YP_001780640.1 MarR family transcriptional regulator [Clostridium perfringens] >gb YP_001780640.1	54.3	3e-06	G
ref YP_001033131.1 MarR family transcriptional regulator [Lactococcus lactis subsp. lactis] [MarR family]	53.9	4e-06	G
ref ZP_02617530.1 transcriptional regulator, MarR family [Clostridium perfringens] >gb ZP_02617530.1	53.9	4e-06	G
ref YP_861960.1 MarR family transcriptional regulator [Gram-negative bacteria] [MarR family]	53.9	4e-06	G
ref NP_391388.1 hypothetical protein BSU35080 [Bacillus subtilis] [MarR family]	53.5	5e-06	G
ref ZP_02994615.1 hypothetical protein CLOSP0_01734 [Clostridium perfringens] >gb ZP_02994615.1	53.5	6e-06	G
ref ZP_01994128.1 hypothetical protein DORLON_00120 [Dorea longata] [MarR family]	53.1	6e-06	G
ref ZP_03294064.1 hypothetical protein CLOHIR_02015 [Clostridium perfringens] >gb ZP_03294064.1	53.1	7e-06	G
ref ZP_02311326.1 hypothetical protein CLOBAR_00939 [Clostridium perfringens] >gb ZP_02311326.1	52.4	1e-05	G
ref YP_001390364.1 MarR family transcriptional regulator [Clostridium perfringens] >gb YP_001390364.1	52.4	1e-05	G
ref YP_0017856407.1 MarR family transcriptional regulator [Clostridium perfringens] >gb YP_0017856407.1	51.6	2e-05	G
ref YP_508725.1 transcriptional regulator [Lactococcus lactis subsp. lactis] [MarR family]	51.2	2e-05	G
ref YP_001628248.1 MarR family transcriptional regulator [Lysinibacillus sphaericus] [MarR family]	51.2	3e-05	G
ref NP_266864.1 transcription regulator [Lactococcus lactis subsp. lactis] [MarR family]	51.2	3e-05	G
ref ZP_01723095.1 transcriptional regulator, MarR family protein [Lysinibacillus sphaericus] [MarR family]	50.4	4e-05	G
ref YP_008147.1 transcriptional regulator [Lactococcus lactis subsp. lactis] [MarR family]	50.4	5e-05	G
ref NP_785298.1 transcription regulator [Lactobacillus plantarum] [MarR family]	50.1	6e-05	G
ref YP_757477.1 MarR family transcriptional regulator [Maricoccus sp.] [MarR family]	50.1	6e-05	G
ref NP_391385.1 hypothetical protein BSU35050 [Bacillus subtilis] [MarR family]	50.1	6e-05	G
ref NP_111681.1 transcription regulator (SlyA-related) [Thermus thermophilus HB8] [MarR family]	49.7	7e-05	G
ref NP_419215.1 MarR family transcriptional regulator [Caulobacter crescentus] [MarR family]	49.3	9e-05	G
ref YP_001031482.1 MarR family transcriptional regulator [Lactococcus lactis subsp. lactis] [MarR family]	49.3	1e-04	G
ref NP_603578.1 MarR family transcriptional regulator [Fusobacterium nucleatum] [MarR family]	48.9	1e-04	G
ref YP_136815.1 MarR family transcriptional regulator [Streptococcus pneumoniae] [MarR family]	48.9	1e-04	G
ref YP_002169566.1 possible MarR family transcriptional regulator [Fusobacterium nucleatum] [MarR family]	48.9	1e-04	G
ref ZP_00144671.1 Transcriptional regulator, MarR family [Fusobacterium nucleatum] [MarR family]	48.9	1e-04	G

Annex 1

<u>ref YP_819912.1 </u>	MarR family transcriptional regulator [Strep...]	46.9	1e-04	G
<u>ref YP_079349.1 </u>	transcriptional regulator YvmB [Bacillus lic...]	46.5	2e-04	G
<u>ref ZP_01219563.1 </u>	putative transcriptional regulator, MarR f...	45.1	2e-04	
<u>ref YP_091756.1 </u>	YvmB [Bacillus licheniformis ATCC 14580] >gb...	45.1	2e-04	G
<u>ref YP_129221.1 </u>	MarR family transcriptional regulator [Photo...]	45.1	2e-04	G
<u>ref ZP_00990845.1 </u>	hypothetical transcriptional regulator, Ma...	45.1	2e-04	
<u>ref YP_001319891.1 </u>	MarR family transcriptional regulator [Al...]	45.8	3e-04	G
<u>ref YP_001838202.1 </u>	MarR family transcriptional regulator [Le...]	45.8	3e-04	G
<u>ref YP_106851.1 </u>	putative transcriptional regulatory protein ...	47.4	4e-04	G
<u>ref YP_0019261680.1 </u>	Transcriptional regulator, marR family [L...	47.4	4e-04	G
<u>ref YP_001310724.1 </u>	MarR family transcriptional regulator [Cl...]	47.4	4e-04	G
<u>ref ZP_01085869.1 </u>	hypothetical transcriptional regulator, Ma...	47.0	5e-04	
<u>ref YP_1407229.1 </u>	MarR family transcriptional regulator [Strep...]	47.0	5e-04	G
<u>ref YP_1433999.1 </u>	MarR family transcriptional regulator [Therm...]	46.6	6e-04	G
<u>ref YP_293371.1 </u>	regulatory protein, MarR [Ralstonia eutropha...]	46.6	7e-04	G
<u>ref YP_001307422.1 </u>	MarR family transcriptional regulator [Cl...]	46.6	7e-04	G
<u>ref ZP_02950515.1 </u>	transcriptional regulator, MarR family [Cl...]	46.2	8e-04	
<u>ref NP_268268.1 </u>	transcription regulator [Lactococcus lactis ...]	46.2	0.001	G
<u>ref YP_002355389.1 </u>	transcriptional regulator, MarR family [D...]	46.2	0.001	G
<u>ref ZP_01684155.1 </u>	probable marR-family transcription regulat...	46.2	0.001	
<u>ref YP_773250.1 </u>	MarR family transcriptional regulator [Burkh...]	45.8	0.001	G
<u>ref ZP_01131766.1 </u>	transcriptional regulator, MarR family pro...	45.8	0.001	
<u>ref ZP_00238819.1 </u>	transcriptional regulator, MarR family [Ba...]	45.6	0.001	
<u>ref YP_002467440.1 </u>	transcriptional regulator, MarR family [C...]	45.6	0.001	G
<u>ref ZP_02547491.1 </u>	hypothetical protein BLAHAN_01259 [Blautia...]	45.4	0.001	
<u>ref ZP_02891041.1 </u>	transcriptional regulator, MarR family [Bu...]	45.4	0.001	
<u>ref YP_001808132.1 </u>	MarR family transcriptional regulator [Bu...]	45.4	0.001	G
<u>ref ZP_03906301.1 </u>	transcriptional regulator, MarR family [Bu...]	45.4	0.001	
<u>ref ZP_03362986.1 </u>	transcriptional regulator, MarR family pro...	45.4	0.001	
<u>ref NP_377055.1 </u>	MarR family transcriptional regulator [Bacil...	45.4	0.002	G
<u>ref NP_792475.1 </u>	MarR family transcriptional regulator [Clost...	45.4	0.002	G
<u>ref ZP_03570809.1 </u>	transcriptional regulator, MarR family [Bu...]	45.1	0.002	
<u>ref YP_001119315.1 </u>	MarR family transcriptional regulator [Bu...]	45.1	0.002	G
<u>ref YP_002418276.1 </u>	Histone acetyltransferase HPA2 and relate...	45.1	0.002	G
<u>ref ZP_02755848.1 </u>	transcriptional regulator, MarR family pro...	45.1	0.002	
<u>ref YP_433075.1 </u>	MarR family transcriptional regulator [Burkh...]	44.7	0.002	G
<u>ref ZP_03633998.1 </u>	transcriptional regulator, MarR family [Cl...]	44.7	0.002	
<u>ref YP_001374721.1 </u>	MarR family transcriptional regulator [Ba...]	44.7	0.002	G
<u>ref YP_819961.1 </u>	transcriptional regulator [Leuconostoc mesen...	44.7	0.002	G
<u>ref ZP_02027443.1 </u>	hypothetical protein EUBVEN_02713 [Eubacte...]	44.7	0.003	

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>ref|NP_268273.1| **G** zinc transport transcription regulator [Lactococcus lactis subsp. lactis II1403]
 gb|AAK06214.1|AE006439_11 **G** zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis II1403]
 Length=145

GENE ID: 1115793 zitR | zinc transport transcription regulator
 [Lactococcus lactis subsp. lactis II1403] (10 or fewer PubMed links)

Score = 291 bits (744), Expect = 1e-77, Method: Compositional matrix adjust.
 Identities = 145/145 (100%), Positives = 145/145 (100%), Gaps = 0/145 (0%)

Query 1	MSLANQIDQFLGTIMQFAENKHEILLGKCESDKVLTSTQEHIMLLAEQISTNAKIAEKL	60
Sbjct 1	MSLANQIDQFLGTIMQFAENKHEILLGKCESDKVLTSTQEHIMLLAEQISTNAKIAEKL	60
Query 61	KISPAAVTKALKKLQEQLIKSSRATNDERVVWLWSLTEKAVPVAKEHATHHEKTLSTYQE	120
Sbjct 61	KISPAAVTKALKKLQEQLIKSSRATNDERVVWLWSLTEKAVPVAKEHATHHEKTLSTYQE	120
Query 121	LGNKFTDEEQEVISKFLSALTEEFQ	145
	LGNKFTDEEQEVISKFLSALTEEFQ	
Sbjct 121	LGNKFTDEEQEVISKFLSALTEEFQ	145

>ref|YP_811979.1| **G** transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
 gb|ABJ73866.1| **G** Transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
 Length=145

GENE ID: 4433026 LACR_2420 | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 268 bits (685), Expect = 1e-70, Method: Compositional matrix adjust.
Identities = 130/145 (89%), Positives = 141/145 (97%), Gaps = 0/145 (0%)

Query 1	MSLANQIDQFLGTTIMQFAENKHEILLGKCESDVKLTSTQEHILMLAEQISTNAKIAEKL	60
Sbjct 1	MSLANQIDQFLG IMQFAENKHEILLG+CES+VVLSTQEHILM+LA ++STNA+IAE+L	
Query 61	MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMILAAEVSTNARIAEQL	60
Sbjct 61	KISPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE	120
Query 121	KISPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHAAHHEKTLSTYQE	120
Sbjct 121	LGDKFTDEEQKVVISQFLSVLTEEFQ	145
Sbjct 121	LGDKFTDEEQKVVISQFLSVLTEEFQ	145

>ref|YP_001033643.1| **G** transcriptional regulator of the zit operon [Lactococcus lactis subsp. cremoris MG1363]

emb|CAL98965.1| **G** transcriptional regulator of the zit operon [Lactococcus lactis subsp. cremoris MG1363]
Length=145

GENE ID: 4799067 zitR | transcriptional regulator of the zit operon
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 267 bits (682), Expect = 2e-70, Method: Compositional matrix adjust.
Identities = 129/145 (88%), Positives = 141/145 (97%), Gaps = 0/145 (0%)

Query 1	MSLANQIDQFLGTTIMQFAENKHEILLGKCESDVKLTSTQEHILMLAEQISTNAKIAEKL	60
Sbjct 1	MSLANQIDQFLG IMQFAENKHEILLG+CES+VVLSTQEHILM+LA ++STNA+IAE+L	
Query 61	MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMILAAEVSTNARIAEQL	60
Sbjct 61	KISPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE	120
Sbjct 61	KISPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKA+PVAKEH A HHEKTLSTYQE	120
Query 121	KISPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKAIPVAKEHAAHHEKTLSTYQE	120
Sbjct 121	LGDKFTDEEQKVVISQFLSVLTEEFQ	145
Sbjct 121	LGDKFTDEEQKVVISQFLSVLTEEFQ	145

>ref|YP_001034147.1| **G** multiple antibiotic resistance operon transcriptional repressor (MarR), putative [Streptococcus sanguinis SK36]

gb|ABN43597.1| **G** Multiple antibiotic resistance operon transcriptional repressor (MarR), putative [Streptococcus sanguinis SK36]
Length=147

GENE ID: 4806188 adcR | multiple antibiotic resistance operon transcriptional repressor (MarR), putative [Streptococcus sanguinis SK36]
(10 or fewer PubMed links)

Score = 154 bits (389), Expect = 2e-36, Method: Compositional matrix adjust.
Identities = 78/142 (54%), Positives = 102/142 (71%), Gaps = 0/142 (0%)

Query 3	LANQIDQFLGTTIMQFAENKHEILLGKCESDVKLTSTQEHILMLAEQISTNAKIAEKLKI	62
Sbjct 4	LAQKIDQFLNEVILKAENQHEILIGSCTSDVPLNTQEHILMLSEESLNSDLAKKLNV	63
Query 63	SPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG	122
Sbjct 64	S AAVTKA+K L QE+++ + D RV + LTE A P+AKEH HH TL TYQ+L	
Sbjct 64	SQAAVTAVKSLARQEMLQAFKDQRDARVTYRLTELAQPIAKEHQHHAAHTLETYQKLA	123
Query 123	NKFTDEEQEVISKFLSALTEEF	144
Sbjct 124	+F+ EQ VI+KFL AL E	
Sbjct 124	EQFSASEQAVIAKFLEALVGEI	145

>ref|NP_722293.1| **G** putative transcriptional regulator [Streptococcus mutans UA159]

gb|AAN59599.1|AE015022_6 **G** putative transcriptional regulator [Streptococcus mutans UA159]
Length=148

GENE ID: 1029245 SMU.1995c | putative transcriptional regulator
[Streptococcus mutans UA159] (10 or fewer PubMed links)

Score = 145 bits (365), Expect = 1e-33, Method: Compositional matrix adjust.
Identities = 76/146 (52%), Positives = 105/146 (71%), Gaps = 1/146 (0%)

Query 1	MSLANQIDQFLGTTIMQFAENKHEILLGKCESDVKLTSTQEHILMLAEQIS-TNAKIAEK	59
Sbjct 1	M+L QID + I+ AEN HE+L+G C+SDVKLT+TQEHILML++ S TN+ +A++	
Query 60	MTLGQQIDALINQIILKAENHHELLIGSCQSDVVLNTQEHILMLLSQEKSNTNSDLAKE	60
Sbjct 61	LKISPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQ	119
Sbjct 61	L IS AAVTKA+K L QE+++ + D RV + LT+ A PVAKEH HH TLS Y	
Query 120	LNISQAATVAVKAVKSLVGQEMLELIKDGTDARVTYRFLTKLAEPVAKEHHHHVATLSYD	120
Sbjct 121	ELGNKFTDEEQEVISKFLSALTEEFQ	145
Sbjct 121	+ KE+ +E+ VIS+FL+ALT+E +	
Sbjct 121	RISQKFSQKEKSVISRFLTALTKELE	146

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>ref|YP_002122498.1| G transcriptional repressor AdcR for Zn(2+)-responsive expression [Streptococcus equi subsp. zooepidemicus MGCS10565]

gb|ACG61485.1| G transcriptional repressor AdcR for Zn(2+)-responsive expression [Streptococcus equi subsp. zooepidemicus MGCS10565]
Length=147

GENE ID: 6760627 adcR | transcriptional repressor AdcR for Zn(2+)-responsive expression [Streptococcus equi subsp. zooepidemicus MGCS10565]

Score = 143 bits (361), Expect = 3e-33, Method: Compositional matrix adjust.
Identities = 70/143 (48%), Positives = 102/143 (71%), Gaps = 0/143 (0%)

Query 3	LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHI L ++D + I+ AEN+HE+L G C+SDVKLT+TQEHI Sbjct 4 LEKKLDNLVNRILLKAENQHELLFGACQS Length=147	MLLAEQISTNAKIAEKLK 62 MLL+TN +A++L I MLLNTQEHILMLLSQEKLTNTDLAKRLNI 63
Query 63	SPAAVTKALKKLQEQLIKSSRATNDERVVLWSL S AAVTKA+K L +QE++ ++ T D RV + LT+ A P+AKEH Sbjct 64 SQAAVTKAIAKGLIKQEMLAGTKDTVDARV Length=147	TEKAVPVAKEHATHHEKTLSTYQELG 122 HH+KTL+ Y L TDLARPIAKEHTHHHDKTLAVYHRL 123
Query 123	NKFDTDEEQEVISKFLSALTEEFQ 145 F+ EEQ ++ KF++A +EE + Sbjct 124 AHFSAAEQVIVEKFITAFSEELE 146	

>ref|NP_606407.1| G putative repressor protein [Streptococcus pyogenes MGAS8232]
ref|NP_663873.1| G putative repressor protein [Streptococcus pyogenes MGAS315]
ref|NP_801332.1| G putative repressor protein [Streptococcus pyogenes SSI-1]
20 more sequence titles

ref YP_059443.1 G MarR family transcriptional regulator [Streptococcus pyogenes MGAS10394]	
ref YP_279544.1 G MarR family transcriptional regulator [Streptococcus pyogenes MGAS6180]	
ref YP_595809.1 G MarR family transcriptional regulator [Streptococcus pyogenes MGAS9429]	
ref YP_597688.1 G MarR family transcriptional regulator [Streptococcus pyogenes MGAS10270]	
ref YP_599676.1 G MarR family transcriptional regulator [Streptococcus pyogenes MGAS2096]	
ref YP_601578.1 G Transcriptional regulator, MarR family [Streptococcus pyogenes MGAS10750]	
ref YP_001127671.1 G MarR family regulatory protein [Streptococcus pyogenes str. Manfredo]	
ref YP_002285129.1 G Putative repressor protein [Streptococcus pyogenes NZ131] sp Q5XEA3.1 ADCR STRP6 RecName: Full=Transcriptional repressor adcR	
gb AAL96906.1 G putative repressor protein [Streptococcus pyogenes MGAS8232]	
gb AAM78676.1 G putative repressor protein [Streptococcus pyogenes MGAS315]	
dbj BAC63165.1 G putative repressor protein [Streptococcus pyogenes SSI-1]	
gb AAT86260.1 G Transcriptional regulator, MarR family [Streptococcus pyogenes MGAS10394]	
gb AAX71189.1 G transcriptional regulator, MarR family [Streptococcus pyogenes MGAS6180]	
gb ABF31265.1 G transcriptional regulator, MarR family [Streptococcus pyogenes MGAS9429]	
gb ABF33144.1 G Transcriptional regulator, MarR family [Streptococcus pyogenes MGAS10270]	
gb ABF35132.1 G Transcriptional regulator, MarR family [Streptococcus pyogenes MGAS2096]	
gb ABF37034.1 G Transcriptional regulator, MarR family [Streptococcus pyogenes MGAS10750]	
emb CAM29417.1 G MarR-family regulatory protein [Streptococcus pyogenes str. Manfredo]	
gb ACI60434.1 G Putative repressor protein [Streptococcus pyogenes NZ131]	

Length=147

GENE ID: 994164 adcR | putative repressor protein [Streptococcus pyogenes MGAS8232] (10 or fewer PubMed links)

Score = 141 bits (356), Expect = 1e-32, Method: Compositional matrix adjust.
Identities = 69/144 (47%), Positives = 101/144 (70%), Gaps = 0/144 (0%)

Query 2	SLANQIDQFLGTIMQFAENKHEILLGKCESDV L ++D + TI+ AEN+HE+L G C+SDVKLT+TQEHI Sbjct 3 TLEKKLDNLVNTILLKAENQHELLFGACQS Length=147	MLLAEQISTNAKIAEKLK 61 MLL+TN +A+ L MLLNTQEHILMLLSQQR 62
Query 62	ISPAAVTKALKKLQEQLIKSSRATNDERV IS AAVTKA+K L +QE++ ++ T D RV + LTE A P+A EH Sbjct 63 ISQAAVTKAIAKSLVKQDMLAGTKDTVDARV Length=147	TEKAVPVAKEHATHHEKTLSTYQEL 121 HH+TL+ Y L TDLAKPIASEHTHHDET 122
Query 122	GNKFTDDEEQEVISKFLSALTEEFQ 145 KF+ +E E++ KF++ EE + Sbjct 123 LQKFSAKELEIVDKFVTVFAEELE 146	

>ref|ZP_02920004.1| hypothetical protein STRINF_00865 [Streptococcus infantarius]

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subsp. infantarius ATCC BAA-102]
 gb|EDT48012.1| hypothetical protein STRINF_00865 [Streptococcus infantarius
 subsp. infantarius ATCC BAA-102]
 Length=148

Score = 141 bits (355), Expect = 2e-32, Method: Compositional matrix adjust.
 Identities = 70/145 (48%), Positives = 103/145 (71%), Gaps = 0/145 (0%)

Query 1 MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60
 Sbjct 1 M_L QID + I+ AEN+HE+L G C+S V+LT+TQEHIMLL++ TN+ +A++L 60
 Query 61 KISPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE 120
 IS AAVTKA+K L ++ ++ + +D RV + LTE A PVA EH HH TLS Y++ 120
 Sbjct 61 NISQAAVTKAIKCLVKEGMLAPVKNKDARVTVFELTEFAKPVADEHNHHHHATLSVYKK 120
 Query 121 LGNKFTDEEQEVISKFLSALTEEFQ 145
 + + F+DEEQ +IS+FL+A ++E +
 Sbjct 121 MIDDFSDEEQSIISRFILTAFSDELE 145

>ref|NP_268489.1| **G** putative repressor protein [Streptococcus pyogenes M1 GAS]
 ref|YP_281441.1| **G** MarR family transcriptional regulator [Streptococcus pyogenes
 MGAS5005]
 gb|AAK33210.1| **G** putative repressor protein [Streptococcus pyogenes M1 GAS]
 gb|AAZ50696.1| **G** transcriptional regulator, MarR family [Streptococcus pyogenes
 MGAS5005]
 Length=147

GENE ID: 900432 adcR | putative repressor protein
 [Streptococcus pyogenes M1 GAS] (10 or fewer PubMed links)

Score = 141 bits (355), Expect = 2e-32, Method: Compositional matrix adjust.
 Identities = 69/143 (48%), Positives = 100/143 (69%), Gaps = 0/143 (0%)

Query 3 LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI 62
 Sbjct 4 L ++D + TI+ AEN+HE+L G C+S DVKLT+TQEHIMLL++O TN +A+ L I 63
 Query 63 SPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG 122
 S AAVTKA+K L +Q+++ ++ T D RV + LTE A P+A EH HH++TL+ Y L 122
 Sbjct 64 SQAAVTKAIKSLVKQDMLLAGTKDTVDARVTVFELTELAKPIASEHTHHHDETLNVYNRLL 123
 Query 123 NKFTDEEQEVISKFLSALTEEFQ 145
 KF+ +E E++ KF++ EE +
 Sbjct 124 QKFSAKELEIVDKFVTVFAEELE 146

>ref|YP_002561480.1| **G** MarR-family regulatory protein [Streptococcus uberis 0140J]
 emb|CAR40515.1| **G** MarR-family regulatory protein [Streptococcus uberis 0140J]
 Length=147

GENE ID: 7392663 SUB0110 | MarR-family regulatory protein
 [Streptococcus uberis 0140J]

Score = 138 bits (348), Expect = 1e-31, Method: Compositional matrix adjust.
 Identities = 69/143 (48%), Positives = 102/143 (71%), Gaps = 0/143 (0%)

Query 3 LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI 62
 Sbjct 4 L ++IDQ + I+ AEN+HE+L G C+S VKLT+TQEHIMLL++ TN +A+KL I 63
 Query 63 SPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG 122
 S AAVTKA+K L + E++ + T D RV + LT A P+A+EH HH++TL+ Y +L 122
 Sbjct 64 SQAAVTKAIKSLMKHEMLSIAIKDTVDARVTVFELTPAAKPIAEHTQHHDETLNVYTKLL 123
 Query 123 NKFTDEEQEVISKFLSALTEEFQ 145
 + F+ EE+ VI KFL+ ++E +
 Sbjct 124 SSFSSEEKAVIDKFLTVFSDELE 146

>ref|NP_687190.1| **G** adc operon repressor AdcR [Streptococcus agalactiae 2603V/R]
 ref|NP_734620.1| **G** adc operon repressor AdcR [Streptococcus agalactiae NEM316]
 ref|YP_328885.1| **G** adc operon repressor AdcR [Streptococcus agalactiae A909]
 13 more sequence titles

ref|ZP_00781732.1| repressor protein adcR [Streptococcus agalactiae 18RS21]
 ref|ZP_00784062.1| adc operon repressor AdcR [Streptococcus agalactiae H36B]
 ref|ZP_00786322.1| adc operon repressor AdcR [Streptococcus agalactiae COH1]
 ref|ZP_00787320.1| adc operon repressor AdcR [Streptococcus agalactiae CJB111]
 ref|ZP_00790981.1| adc operon repressor AdcR [Streptococcus agalactiae 515]
 gb|AAM99062.1|AE014198_10 **G** adc operon repressor AdcR [Streptococcus agalactiae 2603V/R]
 emb|CAD45795.1| **G** unknown [Streptococcus agalactiae NEM316]
 gb|ABA46120.1| **G** adc operon repressor AdcR [Streptococcus agalactiae A909]
 gb|EA061676.1| repressor protein adcR [Streptococcus agalactiae 18RS21]
 gb|EA070283.1| adc operon repressor AdcR [Streptococcus agalactiae 515]
 gb|EA073974.1| adc operon repressor AdcR [Streptococcus agalactiae CJB111]
 gb|EA074935.1| adc operon repressor AdcR [Streptococcus agalactiae COH1]
 gb|EA077202.1| adc operon repressor AdcR [Streptococcus agalactiae H36B]
 Length=147

Annex 1

GENE ID: 1012928 adcR | adc operon repressor AdcR
[Streptococcus agalactiae 2603V/R] (10 or fewer PubMed links)

Score = 136 bits (343), Expect = 5e-31, Method: Compositional matrix adjust.
Identities = 65/143 (45%), Positives = 99/143 (69%), Gaps = 0/143 (0%)

Query 3	LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHIMLLAEQISTNAKIAEKLIK I	62
Sbjct 4	L + ++D + I+ AEN+HE+L G C +SDVKLT+TQEHIMLL++ TN+ +A+KL I	
Query 63	LEQKLDHLVSQILLKAENQHELLFGTCQSVDVKTNTQEHIMLLSEQQLTNSDLAKKLNI	63
Sbjct 64	SPAAVTALKKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG S	122
Query 123	AAVTKA+K L Q+++K+++ + D R+ + L+E A P+A EH HH+ TL Y L	
Sbjct 124	SQAAVTAVKSLISQDMLKANKDSKDARITYFELSELAKPIADEHHTHHDTNLGVYGR LV	123
Query 123	NKFTDEEQEVISKFLSALTEEFQ N F+ +E+ V+ +FL + E +	145
Sbjct 124	NHFSKDEKVVLERFLDLFSRELE	146

>ref|YP_001451205.1| **G** repressor protein adcR [Streptococcus gordonii str. Challis substr. CH1]
gb|AAO43167.1| putative transcriptional repressor; AdcR [Streptococcus gordonii subsp. challis]
gb|ABV10972.1| **G** repressor protein adcR [Streptococcus gordonii str. Challis substr. CH1]
Length=147

GENE ID: 5599115 adcR | repressor protein adcR
[Streptococcus gordonii str. Challis substr. CH1] (10 or fewer PubMed links)

Score = 133 bits (335), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 75/142 (52%), Positives = 101/142 (71%), Gaps = 0/142 (0%)

Query 3	LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHIMLLAEQISTNAKIAEKLIK I	62
Sbjct 4	LA++ID FL I+ AEN+HEIL+G C S+V LT+TQEHIMLLAE++ TN+ +A+KL +	
Query 63	LAHKIDSFLNEIILKAENQHEILVGSCTSNVALTNTQEHIMLLAEEMLTNSDLAKKL NI	63
Sbjct 64	SPAAVTALKKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG S	122
Query 123	AAVTKA+K L Q ++++ + D RV+ + LTE A P+A EH HH TL TYQ L	
Sbjct 124	SQAAVTAVKSLINQGMLETFKDKKDARVTFYRLTELAQPIADEHEHHHAHTLETYQSL L	123
Query 123	NKFTDEEQEVISKFLSALTEEF ++F+ +E+ I KFL AL E	144
Sbjct 124	DRFSQDEQQAIKFLEALVGEI	145

>ref|ZP_01817760.1| adc operon repressor AdcR [Streptococcus pneumoniae SP3-BS71]
ref|YP_002512031.1| **G** MarR-family regulatory protein [Streptococcus pneumoniae ATCC 700669]
gb|EDK74363.1| adc operon repressor AdcR [Streptococcus pneumoniae SP3-BS71]
emb|CAR69937.1| **G** MarR-family regulatory protein [Streptococcus pneumoniae ATCC 700669]
Length=146

Score = 132 bits (333), Expect = 6e-30, Method: Compositional matrix adjust.
Identities = 71/143 (49%), Positives = 106/143 (74%), Gaps = 0/143 (0%)

Query 3	LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHIMLLAEQISTNAKIAEKLIK I	62
Sbjct 4	LA ID FL ++ AEN+HEIL+G C S+V LT+TQEHIMLL+E+ TN++A +L +	
Query 63	LAKDIDAFLNEVILQAENQHEILIGHCTSEVALNTNTQEHIMLLSEESLTNSELARRLN V	63
Sbjct 64	SPAAVTALKKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG S	122
Query 123	AAVTKA+K L ++ ++++ + D RV+ + LT+ A P+A+EH HHE TL TY++	
Sbjct 124	SQAAVTAVKSLVKEGMLETSKDSKDARVIFYQLTDLARPIAEEHHHHHEHTLLTYEQVA	123
Query 123	NKFTDEEQEVISKFLSALTEEFQ +FT EQ+VI +FL+AL E +	145
Sbjct 124	TQFTPNEQKVIQRFLTALVGEIK	146

>ref|NP_359569.1| **G** adc operon repressor AdcR [Streptococcus pneumoniae R6]
ref|ZP_01825537.1| Transcriptional repressor for Zn(2+)-responsive expression [Streptococcus pneumoniae SP11-BS70]
ref|YP_001836857.1| **G** adc operon repressor AdcR [Streptococcus pneumoniae CGSP14]
ref|ZP_02964427.1| putative transcriptional repressor [Streptococcus pneumoniae CDC0288-04]
gb|AAL00780.1| **G** Transcriptional repressor for Zn(2+)-responsive expression [Streptococcus pneumoniae R6]
gb|EDK63077.1| Transcriptional repressor for Zn(2+)-responsive expression [Streptococcus pneumoniae SP11-BS70]
gb|ACB91392.1| **G** adc operon repressor AdcR [Streptococcus pneumoniae CGSP14]
gb|EDT94590.1| putative transcriptional repressor [Streptococcus pneumoniae CDC0288-04]
Length=166

GENE ID: 933868 adcR | adc operon repressor AdcR [Streptococcus pneumoniae R6]
(10 or fewer PubMed links)

Score = 131 bits (329), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 70/143 (48%), Positives = 106/143 (74%), Gaps = 0/143 (0%)

Query 3	LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHIMLLAEQISTNAKIAEKLIK I	62
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Annex 1

Sbjct 24 LA I+ FL ++ AEN+HEIL+G C S+v LT+TQEHIMLL+E+ TN++A +L + LAKDINAFLNEVILQAENQHEILIGHCTSEVALNTQEHILMLLSEESLTNSELARRLNV 83

Query 63 SPAAVTKALKLQEQLIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSYQELG 122
S AAVTKA+K L ++ +++S+ + D RV+ + LT+ A P+A+EH HHE TL TY++
Sbjct 64 SQAAVTKAIAKSLVKEGMLETSKDSKDARVIFYQLTDLARPIAEHHHHHEHTLLTYEQVA 123

Query 123 NKFTDEEQEVISKFLSALTEEFQ 145
+FT EQ+VI +FL+AL E +
Sbjct 144 TQFTPNEQKVIQRFLTALVGEIK 146

>ref|NP_346586.1| **G** adc operon repressor AdcR [Streptococcus pneumoniae TIGR4]
ref|ZP_01408975.1| **G** hypothetical protein SpneT_02000553 [Streptococcus pneumoniae TIGR4]
ref|YP_817386.1| **G** adc operon repressor AdcR [Streptococcus pneumoniae D39]
29 more sequence titles

ref|ZP_01820229.1| adc operon repressor AdcR [Streptococcus pneumoniae SP6-BS73]
ref|ZP_01821749.1| adc operon repressor AdcR [Streptococcus pneumoniae SP9-BS68]
ref|ZP_01827937.1| adc operon repressor AdcR [Streptococcus pneumoniae SP14-BS69]
ref|ZP_01830531.1| adc operon repressor AdcR [Streptococcus pneumoniae SP18-BS74]
ref|ZP_01833186.1| adc operon repressor AdcR [Streptococcus pneumoniae SP19-BS75]
ref|ZP_01835060.1| adc operon repressor AdcR [Streptococcus pneumoniae SP23-BS72]
ref|ZP_02708953.1| putative transcriptional repressor [Streptococcus pneumoniae CDC1873-00]
ref|ZP_02710784.1| putative transcriptional repressor [Streptococcus pneumoniae CDC1087-00]
ref|ZP_02713441.1| putative transcriptional repressor [Streptococcus pneumoniae SP195]
ref|ZP_02718213.1| putative transcriptional repressor [Streptococcus pneumoniae CDC3059-06]
ref|ZP_02721950.1| putative transcriptional repressor [Streptococcus pneumoniae MLV-016]
ref|YP_001695528.1| **G** putative transcriptional repressor [Streptococcus pneumoniae HungaryI9A-6]
ref|YP_002038763.1| **G** transcriptional regulator, MarR family [Streptococcus pneumoniae G54]
emb|CAA96184.1| AdcR protein [Streptococcus pneumoniae]
gb|AAK76226.1| **G** adc operon repressor AdcR [Streptococcus pneumoniae TIGR4]
gb|ABJ54931.1| **G** adc operon repressor AdcR [Streptococcus pneumoniae D39]
gb|EDK65765.1| adc operon repressor AdcR [Streptococcus pneumoniae SP14-BS69]
gb|EDK68416.1| adc operon repressor AdcR [Streptococcus pneumoniae SP18-BS74]
gb|EDK70926.1| adc operon repressor AdcR [Streptococcus pneumoniae SP19-BS75]
gb|EDK76701.1| adc operon repressor AdcR [Streptococcus pneumoniae SP6-BS73]
gb|EDK80035.1| adc operon repressor AdcR [Streptococcus pneumoniae SP9-BS68]
gb|EDK81745.1| adc operon repressor AdcR [Streptococcus pneumoniae SP23-BS72]
gb|ACA36761.1| **G** putative transcriptional repressor [Streptococcus pneumoniae HungaryI9A-6]
gb|EDT50754.1| putative transcriptional repressor [Streptococcus pneumoniae CDC1873-00]
gb|EDT91227.1| putative transcriptional repressor [Streptococcus pneumoniae CDC1087-00]
gb|EDT92758.1| putative transcriptional repressor [Streptococcus pneumoniae SP195]
gb|EDT96372.1| putative transcriptional repressor [Streptococcus pneumoniae CDC3059-06]
gb|EDT98576.1| putative transcriptional repressor [Streptococcus pneumoniae MLV-016]
gb|ACF56415.1| **G** transcriptional regulator, MarR family [Streptococcus pneumoniae G54]
Length=146

GENE ID: 931929 SP 2172 | adc operon repressor AdcR [Streptococcus pneumoniae TIGR4] (10 or fewer PubMed links)

Score = 130 bits (328), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 70/143 (48%), Positives = 106/143 (74%), Gaps = 0/143 (0%)

Query 3 LANQIDQFLGTIMQFAENKHEILLGKCESDVKLSTQEHILMLLAEQISTNAKIAEKLI 62
Sbjct 4 LA I+ FL ++ AEN+HEIL+G C S+v LT+TQEHIMLL+E+ TN++A +L + LAKDINAFLNEVILQAENQHEILIGHCTSEVALNTQEHILMLLSEESLTNSELARRLNV 63

Query 63 SPAAVTKALKLQEQLIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSYQELG 122
S AAVTKA+K L ++ +++S+ + D RV+ + LT+ A P+A+EH HHE TL TY++
Sbjct 64 SQAAVTKAIAKSLVKEGMLET SKDSKDARVIFYQLTDLARPIAEHHHHHEHTLLTYEQVA 123

Query 123 NKFTDEEQEVISKFLSALTEEFQ 145
+FT EQ+VI +FL+AL E +
Sbjct 124 TQFTPNEQKVIQRFLTALVGEIK 146

>ref|YP_138725.1| **G** zinc transport transcriptional repressor [Streptococcus thermophilus LMG 183T1]
ref|YP_140614.1| **G** zinc transport transcriptional repressor [Streptococcus thermophilus CNRZ1066]
gb|AAV59910.1| **G** zinc transport transcriptional repressor [Streptococcus thermophilus LMG 18311]
gb|AAV61799.1| **G** zinc transport transcriptional repressor [Streptococcus thermophilus CNRZ1066]

Length=151

GENE ID: 3164452 adcR | zinc transport transcriptional repressor [Streptococcus thermophilus LMG 18311] (10 or fewer PubMed links)

Score = 129 bits (325), Expect = 5e-29, Method: Compositional matrix adjust.
Identities = 62/145 (42%), Positives = 104/145 (71%), Gaps = 0/145 (0%)

Query 1	MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLSTQEHILMLLAEQISTNAKIAEKL	60
Sbjct 6	+ L Q++Q + I+ AEN++E+L+G+C S VKLT+TQEHIMLL+E TN+++A+ L IELEEEVNQLINQILLKAENQYELLIGQCRSKVVLNTQEHILMLLSEGQKTNSELAKAL	65
Query 61	KISPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE	120
Sbjct 66	+S AAVTKA+K L ++ +++ + +D RV + LT++A P+A+EH HH++TL Y+ NVSQAAVTKAVKTLVKEGMLEGKKDKDDGRVTYFVLTQEAQPIAQEHKEHHQETLGVYRS	125
Query 121	LGNKFTDEEQEVISKFLSALTEEFQ	145
Sbjct 126	+ ++F +E++VI +FL L E+ + VLDQFDHQERQVIGRFLIKLAEKIE	150

>**ref|YP_819746.1| G zinc transport transcriptional repressor [Streptococcus thermophilus LMD-9]**

gb|ABJ65550.1| G transcriptional regulator, MarR family [Streptococcus thermophilus LMD-9]
Length=147

GENE ID: 4438531 STER_0233 | zinc transport transcriptional repressor [Streptococcus thermophilus LMD-9] (10 or fewer PubMed links)

Score = 128 bits (322), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 61/145 (42%), Positives = 104/145 (71%), Gaps = 0/145 (0%)

Query 1	MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLSTQEHILMLLAEQISTNAKIAEKL	60
Sbjct 2	+ L +++Q + I+ AEN++E+L+G+C S VKLT+TQEHIMLL+E TN+++A+ L IELEERVNQLINQILLKAENQYELLIGQCRSKVVLNTQEHILMLLSEGQKTNSELAKAL	61
Query 61	KISPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE	120
Sbjct 62	+S AAVTKA+K L ++ +++ + +D RV + LT++A P+A+EH HH++TL Y+ NVSQAAVTKAVKTLVKEGMLEGKKDKDDGRVTYFVLTQEAQPIAQEHKEHHQETLGVYRS	121
Query 121	LGNKFTDEEQEVISKFLSALTEEFQ	145
Sbjct 122	+ ++F +E++VI +FL L E+ + VLDQFDHQERQVIGRFLIKLAEKIE	146

>**ref|YP_001197479.1| G transcriptional regulator [Streptococcus suis 05ZYH33]**

gb|ABP89079.1| G Transcriptional regulator [Streptococcus suis 05ZYH33]
Length=149

GENE ID: 5099418 SSU05_0109 | transcriptional regulator [Streptococcus suis 05ZYH33] (10 or fewer PubMed links)

Score = 116 bits (290), Expect = 7e-25, Method: Compositional matrix adjust.
Identities = 70/143 (48%), Positives = 100/143 (69%), Gaps = 0/143 (0%)

Query 3	LANQIDQFLGTIMQFAENKHEILLGKCESDVKLSTQEHILMLLAEQISTNAKIAEKLKI	62
Sbjct 6	+A +I+++L I+ +EN+ EIL+G C+S VKLT+TQEHIML+ + TN +IA++L + IALEIEYLHEIVLSSSENQLEILVGSCQSTVKLTNTQEHILMLIEKAAYTNTEIAKELNV	65
Query 63	SPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG	122
Sbjct 66	S AA+TKA K L Q L+ + R D R+V +SLTE A P+A EHA HH TL Y+EL SQAAITKATKSLVAQGLLVAVRDDKDARIVRFSLTEAAKPIAAEHAAHHAAHTLEAYEELL	125
Query 123	NKFTDEEQEVISKFLSALTEEFQ	145
Sbjct 126	+ EEQE I++FLS L E+ + ENYSLEEQQESIARFLSELVEKIR	148

>**ref|ZP_03625066.1| transcriptional regulator, MarR family [Streptococcus suis 89/1591]**

gb|EEF64628.1| transcriptional regulator, MarR family [Streptococcus suis 89/1591]

Length=149

Score = 110 bits (275), Expect = 4e-23, Method: Compositional matrix adjust.
Identities = 69/140 (49%), Positives = 98/140 (70%), Gaps = 0/140 (0%)

Query 6	QIDQFLGTIMQFAENKHEILLGKCESDVKLSTQEHILMLLAEQISTNAKIAEKLKISPA	65
Sbjct 9	+I+++L I+ +EN+ EIL+G C+S VKLT+TQEHIML+ + TN +IA++L +S A EIEKYLHEIVLSSSENQLEILVGSCQSTVKLTNTQEHILMLIEKAAYTNTEIAKELNVSQA	68
Query 66	AVTKALKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKF	125
Sbjct 69	A+TKA K L Q L+ + R D R+V +SLTE A P+A EHA HH TL Y+EL + AITKATKSLVAQGLLVAVRDDKDARIVRFSLTEAAKPIATEHAHHAAHTLEAYEELLEHY	128
Query 126	TDEEQEVISKFLSALTEEFQ	145
Sbjct 129	+ EEQE I++FLS L E+ + SLEEQQESIARFLSELVEKIR	148

>**emb|CAA75313.1| hypothetical protein [Lactococcus lactis subsp. cremoris]**
Length=48

Score = 92.4 bits (228), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 43/47 (91%), Positives = 46/47 (97%), Gaps = 0/47 (0%)

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Query 1 MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLA 47
 Sbjct 1 MSLANQIDQFLG IMQFAENKHEILLG+CES+VVLTSQEHILM+LA 47

>ref|ZP_00365496.1| COG1846: Transcriptional regulators [Streptococcus pyogenes M49 591]
 Length=103

Score = 90.9 bits (224), Expect = 3e-17, Method: Compositional matrix adjust.
 Identities = 45/102 (44%), Positives = 68/102 (66%), Gaps = 0/102 (0%)

Query 44 MLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQLIKSSRATNDERVVLSLTEKAVPV 103
 MLL++Q TN +A+ L IS AAVTKA+K L +Q+++ ++ T D RV + LTE A P+
 Sbjct 1 MLLSQQLRTNTDLAKALNISQAAVTKAISLKVQDMLAGTKDTVDARVTYFELTELAKPI 60

Query 104 AKEHATHHEKTTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ 145
 A EH HH++TL+ Y L KF+ +E E++ KF++ EE +
 Sbjct 61 ASEHTHHHDETLNVYNRNLQKFSAKELEIVDKFVTVFAEELE 102

>ref|YP_001485459.1| **G** MarR family transcriptional regulator [Bacillus pumilus SAFR-032]
 ref|ZP_03056081.1| YvnA [Bacillus pumilus ATCC 7061]
 gb|ABV60899.1| **G** possible MarR family transcriptional regulator [Bacillus pumilus SAFR-032]
 gb|EDW20313.1| YvnA [Bacillus pumilus ATCC 7061]
 Length=152

GENE ID: 5619427 BPUM_0200 | MarR family transcriptional regulator
 [Bacillus pumilus SAFR-032] (10 or fewer PubMed links)

Score = 67.0 bits (162), Expect = 5e-10, Method: Compositional matrix adjust.
 Identities = 40/111 (36%), Positives = 66/111 (59%), Gaps = 2/111 (1%)

Query 36 TSTQEHILMLLAEQI--STNAKIAEKLKISPAAVTKALKKLQEQLIKSSRATNDERVV 93
 T TQ HIL ++ S N ++++LK+S A+TKA+KKL ++ ++ D++ V
 Sbjct 42 TLTQLHILSMIQANPNESNNFLSQQLKLSKPAITKAVKKLIDKGMDYCHRQGDKKS VY 101

Query 94 WSLTEKAVPVAKEHATHHEKTTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
 +SLTEK +A H HEK ++Y E +F ++E +VI +FL A E+
 Sbjct 102 YSLTEKGTQLAALHDELHEKAVASYLEFLQQPHEDELQVIERFLKAWKEKI 152

>ref|YP_001199672.1| **G** transcriptional regulator [Streptococcus suis 98HAH33]
 gb|ABP91272.1| **G** Transcriptional regulator [Streptococcus suis 98HAH33]
 Length=87

GENE ID: 5101832 SSU98_0112 | transcriptional regulator
 [Streptococcus suis 98HAH33] (10 or fewer PubMed links)

Score = 63.2 bits (152), Expect = 6e-09, Method: Compositional matrix adjust.
 Identities = 41/86 (47%), Positives = 56/86 (65%), Gaps = 0/86 (0%)

Query 60 LKISPAAVTKALKKLQEQLIKSSRATNDERVVLSLTEKAVPVAKEHATHHEKTTLSTYQ 119
 + +S AA+TKA K L Q L+ + R D R+V +SLTE A P+ EHA HH TL Y+
 Sbjct 1 MNVSQAATKATKSLVAQGLLVAQRDDKDALIRVRFSLTEAAKPIAAEHHHHAAHTLEAYE 60

Query 120 ELGNKFTDEEQEVISKFLSALTEEFQ 145
 EL ++ EEQE I++FLS L E+ +
 Sbjct 61 ELLENYSLEEQESIARFLSELVEKIR 86

>ref|YP_187318.1| **G** MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus COL]
 ref|YP_495086.1| **G** MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus USA300]
 ref|YP_001576367.1| **G** MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus USA300_TCH1516]
 ref|ZP_02761767.1| **G** MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus USA300_TCH1516]
 gb|AAW37302.1| **G** transcriptional regulator, MarR family [Staphylococcus aureus subsp. aureus COL]
 gb|ABD21126.1| **G** transcriptional regulator, MarR family [Staphylococcus aureus subsp. aureus USA300_FPR3757]
 gb|ABX30488.1| **G** MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus USA300_TCH1516]
 Length=154

GENE ID: 3238188 SACOL2524 | MarR family transcriptional regulator
 [Staphylococcus aureus subsp. aureus COL] (10 or fewer PubMed links)

Score = 63.2 bits (152), Expect = 7e-09, Method: Compositional matrix adjust.
 Identities = 40/112 (35%), Positives = 66/112 (58%), Gaps = 1/112 (0%)

Query 35 LTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQLIKSSRATNDERVV 93
 L+ TQ HI+ L+ N K +E L +S A+TK++KKL ++L+ S ++R V
 Sbjct 36 LS LTQFHIIELIDNNNDKVNNKFLESEMLNVSKPAITKSIKKLLAKDLVVEHNEFNKREVN 95

Query 94 WSLTEKAVPVAKEHATHHEKTTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ 145
 +SLT+K ++ H HEK++ Y+E+ F D+E VI +FL+ EE +
 Sbjct 96 YSLTQKGKKLSSYIHDELHEKSVKKYEEVLKVFDDEMAVIIEFLNRSIEELK 147

>ref|YP_001727325.1| **G** transcriptional repressor for Zn(2+)-responsive expression [Leuconostoc citreum KM20]

gb|ACA81881.1| **G** Transcriptional repressor for Zn(2+)-responsive expression [Leuconostoc citreum KM20]
Length=146

GENE ID: 6063203 adcR | transcriptional repressor for Zn(2+)-responsive expression [Leuconostoc citreum KM20] (10 or fewer PubMed links)

Score = 62.8 bits (151), Expect = 8e-09, Method: Compositional matrix adjust.
Identities = 41/138 (29%), Positives = 72/138 (52%), Gaps = 2/138 (1%)

Query 1	MSLANQIDQFLGTIMQFAENKHEILLGKCESDV--KLTSTQEHLMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKL	60
Sbjct 1	MSQSDHIIQELNTFVQTYASSEFI--QTTAAQKINATQAHLLMLLKTQHATNSSLAESM	58
Query 61	KISPAAVTKALKKLQEQLIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE	120
Sbjct 59	HLTKPAITKAIAKMLIAHGYVVATKDVNDKRSPVNYQLSTEGMQLAAQHEASHRNLLHHRIDH	118
Query 121	LGNKFTDEEQEVISKFLS	138
Sbjct 119	FT ++E I FL+	136

>ref|YP_501277.1| **G** hypothetical protein SAOUHSC_02819 [Staphylococcus aureus subsp. aureus NCTC 8325]

ref|YP_001333445.1| **G** transcriptional regulator MarR family protein [Staphylococcus aureus subsp. aureus str. Newman]

gb|ABD31821.1| **G** conserved hypothetical protein [Staphylococcus aureus subsp. aureus NCTC 8325]

dbj|BAF68683.1| **G** transcriptional regulator MarR family protein [Staphylococcus aureus subsp. aureus str. Newman]
Length=152

GENE ID: 3921258 SAOUHSC_02819 | hypothetical protein [Staphylococcus aureus subsp. aureus NCTC 8325]

Score = 62.8 bits (151), Expect = 8e-09, Method: Compositional matrix adjust.
Identities = 40/112 (35%), Positives = 66/112 (58%), Gaps = 1/112 (0%)

Query 35	LTSTQEHLMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQLIKSSRATNDERVVL	93
Sbjct 34	LSLTQFHIIIELIDNNNDKVNNKFLESEMLNVSKPAITKSIIKKLLAKDLVVEHNEFNKREVN	93
Query 94	WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ	145
Sbjct 94	+SLT+K ++ H HEK++ Y+E+ F D+E VI +FL+ EE + YSLTQKGKKLSYIHDDELHEKSVKKYEEVLKVFDDDEMAVIIEFLNRSIEELK	145

>ref|ZP_03563431.1| MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus str. JKD6008]
ref|ZP_03566444.1| MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus str. JKD6009]
Length=154

Score = 61.2 bits (147), Expect = 3e-08, Method: Compositional matrix adjust.
Identities = 40/112 (35%), Positives = 65/112 (58%), Gaps = 1/112 (0%)

Query 35	LTSTQEHLMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQLIKSSRATNDERVVL	93
Sbjct 36	L+ TQ HI+ L+ N K ++E L +S A+TK++KKL ++L+ S ++R V LSLTQFHIIIELIDNNNDKVNNKFLESEMLNVSKPAITKSIIKKLLAKDLVVEHNEFNKREVN	95
Query 94	WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ	145
Sbjct 96	SLT+K ++ H HEK++ Y+E+ F D+E VI +FL+ EE + CSLTQKGKKLSYIHDDELHEKSVKKYEEVLKVFDDDEMAVIIEFLNRSIEELK	147

>ref|YP_174450.1| **G** MarR family transcriptional regulator [Bacillus clausii KSM-K16]
dbj|BAD63489.1| **G** MarR family transcriptional regulator [Bacillus clausii KSM-K16]
Length=153

GENE ID: 3204362 ABC0950 | MarR family transcriptional regulator [Bacillus clausii KSM-K16] (10 or fewer PubMed links)

Score = 60.5 bits (145), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 40/128 (31%), Positives = 73/128 (57%), Gaps = 3/128 (2%)

Query 18	AENKHEILLGKCESDV--KLTSTQEHLMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKL	74
Sbjct 21	A+ + + + G E + T TQ HI+ ++ EQ + N +AE L +S A+TKA+KKL ADRRRKAMKGQSSEESIVSDWTLTQLHIVAIVKEQERANNTMLAEHLLNVSKPAITKAVKKL	80
Query 75	QEQLIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVIS	134
Sbjct 81	+Q++++ ++ ++++ V + LT+ +A H HE+ + Y + +F E E I LDQQILEKTQQADNKKEVYYRLTKSGEMLAFIHSQQLHEQARNRYMRFIAEFNSTELETII	140
Query 135	KFLSALTE	142
Sbjct 141	+FL AL E	148

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>ref|YP_080661.1| **G** transcriptional regulator YvnA [Bacillus licheniformis ATCC 14580]
 >gb|AAU25023.1| **G** probable transcriptional regulator YvnA [Bacillus licheniformis ATCC 14580]
 Length=157

GENE ID: 3028745 *yvnA* | transcriptional regulator YvnA
 [Bacillus licheniformis ATCC 14580] (10 or fewer PubMed links)

Score = 59.3 bits (142), Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 37/105 (35%), Positives = 64/105 (60%), Gaps = 2/105 (1%)

Query 36	TSTQEHILMLLAEQIS--TNAKIAEKLKISPAAVTKALKLQEELIKSSRATNDERVVL	93
	T TQ HI+ L+E + NA +A KL+IS AAVTKA+ L + I+S + N+ + +	
Sbjct 47	TLTQLHISLISESEADVNNFLAAKLQISKAATKAVNVLTKHGMIESHKKPNNNKELY	106
Query 94	WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS	138
	++LT++ +A H HE Y EL ++F++ E + + +FL+	
Sbjct 107	YTLTDEGKKLADIHDRMHEIAKQRYIELFDRFSESELQTVIRFLN	151

>ref|YP_254603.1| **G** hypothetical protein pSHaeC05 [Staphylococcus haemolyticus JCSC1435]
 >gb|BAE05997.1| **G** unnamed protein product [Staphylococcus haemolyticus JCSC1435]
 Length=155

GENE ID: 3431756 *pSHaeC05* | hypothetical protein
 [Staphylococcus haemolyticus JCSC1435] (10 or fewer PubMed links)

Score = 59.3 bits (142), Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 38/119 (31%), Positives = 69/119 (57%), Gaps = 1/119 (0%)

Query 28	KCESDVKLTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKLQEELIKSSRAT	86
	K D+ L+ TQ HI+ ++ + N K +AE+L +S AVTK+KKL +EL+	
Sbjct 29	KGNEDMDLSLTQFHIIIEIIDKHEKVNNKFIAEELNVSKPAVTKSIKKLSSKELVNLNE	88
Query 87	NDERVVLWLSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ	145
	++R V ++LT++ ++ H H+K + Y+E+ F ++E E I +FL +E +	
Sbjct 89	SNKREVYYNLTKRGEKLSFIHDDLHKVAKVKKYEEVLKFVDEKEMETIIEFLKRSVDELK	147

>ref|YP_093087.1| **G** YvnA [Bacillus licheniformis ATCC 14580]
 >gb|AAU42394.1| **G** YvnA [Bacillus licheniformis DSM 13]
 Length=160

GENE ID: 3100261 *yvnA* | similar to proteins from *B. subtilis*
 [Bacillus licheniformis ATCC 14580] (10 or fewer PubMed links)

Score = 59.3 bits (142), Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 37/105 (35%), Positives = 64/105 (60%), Gaps = 2/105 (1%)

Query 36	TSTQEHILMLLAEQIS--TNAKIAEKLKISPAAVTKALKLQEELIKSSRATNDERVVL	93
	T TQ HI+ L+E + NA +A KL+IS AAVTKA+ L + I+S + N+ + +	
Sbjct 50	TLTQLHISLISESEADVNNFLAAKLQISKAATKAVNVLTKHGMIESHKKPNNNKELY	109
Query 94	WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS	138
	++LT++ +A H HE Y EL ++F++ E + + +FL+	
Sbjct 110	YTLTDEGKKLADIHDRMHEIAKQRYIELFDRFSESELQTVIRFLN	154

>ref|ZP_00738634.1| Transcriptional regulator, MarR family [Bacillus thuringiensis serovar israelensis ATCC 35646]
 >gb|EA057135.1| Transcriptional regulator, MarR family [Bacillus thuringiensis serovar israelensis ATCC 35646]
 Length=156

Score = 55.8 bits (133), Expect = 9e-07, Method: Compositional matrix adjust.
 Identities = 32/106 (30%), Positives = 64/106 (60%), Gaps = 2/106 (1%)

Query 36	TSTQEHILMLLAE--QISTNAKIAEKLKISPAAVTKALKLQEELIKSSRATNDERVVL	93
	T TQ HI+ ++ E Q N ++ +L IS A ++KA++ L + +++ + + T++++ +	
Sbjct 46	TLTQLHIVSVIHESKQQMNNNTLLSMELNISKATISKAIRVLIDNKILLTHQNTDNKKEIF	105
Query 94	WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSA	139
	++LT+K + +A H H+ Y EL +F D E ++++KFL A	
Sbjct 106	YTLTDKGIGQLAIVHKKLHKIAHERYSELFQQFNDSELQIVTKFLEA	151

>ref|ZP_02613091.1| transcriptional regulator, MarR family [Clostridium botulinum NCTC 2916]
 >gb|EDT83321.1| transcriptional regulator, MarR family [Clostridium botulinum NCTC 2916]
 Length=174

Score = 54.3 bits (129), Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 35/113 (30%), Positives = 62/113 (54%), Gaps = 2/113 (1%)

Query 30	ESDVKLTSTQEHILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKLQEELIKSSRATN	87
	++D+K S E H++ + + +S N IA +L ++ + +K KL + + +IK+ + N	
Sbjct 58	DNDIKGISLSEFHVICIGKNNMSNNIFIARELNMTKGGISKINSKLLSKDIIKADKIE	117
Query 88	DERVVLWLSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS	140
	D+R + +SLTEK + + K H HEK ++ + + EE I KFL L	
Sbjct 118	DKREIYYSLTEKGIALFKLHEYLHEKEREKLMKILSNYKLEEITILKFLED	170

>ref|YP_001253547.1| **G** MarR family transcriptional regulator [Clostridium botulinum A str. ATCC 3502]
 ref|YP_001383390.1| **G** MarR family transcriptional regulator [Clostridium botulinum A str. ATCC 19397]
 ref|YP_001386937.1| **G** MarR family transcriptional regulator [Clostridium botulinum A str. Hall]
 emb|CAL82569.1| **G** MarR-family transcriptional regulator [Clostridium botulinum A str. ATCC 3502]
 gb|ABS35317.1| **G** transcriptional regulator, MarR family [Clostridium botulinum A str. ATCC 19397]
 gb|ABS36227.1| **G** transcriptional regulator, MarR family [Clostridium botulinum A str. Hall]
 Length=174

GENE ID: 5185271 CBO1016 | MarR family transcriptional regulator
 [Clostridium botulinum A str. ATCC 3502] (10 or fewer PubMed links)

Score = 54.3 bits (129), Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 35/113 (30%), Positives = 63/113 (55%), Gaps = 2/113 (1%)

Query 30	ESDVVLTLSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKLQEELIKSSRATN	87
	++D+K S E H++ + + +S N IA++L ++ + +K KL +++IK+ + N	
Sbjct 58	DNDIKGISLSEFHVICIGKNNMSNNIFIAKELNMTKGGISKINSKLLSKDIIKADKIEN	117
Query 88	DERVVVLSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL	140
	D+R + +SLTEK + + K H HEK ++ + + EE I KFL L	
Sbjct 118	DKREIYYSLTEKGIALFKLHEHLHEKEREKLMKILSNYKLEEITTILKFLEDL	170

>ref|YP_001780642.1| **G** MarR family transcriptional regulator [Clostridium botulinum B1 str. Okra]
 gb|ACA44681.1| **G** transcriptional regulator, MarR family [Clostridium botulinum B1 str. Okra]
 Length=174

GENE ID: 6149223 CLD_3550 | MarR family transcriptional regulator
 [Clostridium botulinum B1 str. Okra] (10 or fewer PubMed links)

Score = 54.3 bits (129), Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 35/113 (30%), Positives = 63/113 (55%), Gaps = 2/113 (1%)

Query 30	ESDVVLTLSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKLQEELIKSSRATN	87
	++D+K S E H++ + + +S N IA++L ++ + +K KL +++IK+ + N	
Sbjct 58	DNDIKGISLSEFHVICIGKNNMSNNIFIAKELNMTKGGISKINSKLLSKDIIKADKIEN	117
Query 88	DERVVVLSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL	140
	D+R + +SLTEK + + K H HEK ++ + + EE I KFL L	
Sbjct 118	DKREIYYSLTEKGIALFKLHEHLHEKEREKLMKILSNYKLEEITTILKFLEDL	170

>ref|YP_001033131.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
 emb|CAL98430.1| **G** transcriptional regulator, MarR family [Lactococcus lactis subsp. cremoris MG1363]
 Length=295

GENE ID: 4797387 rmaB | MarR family transcriptional regulator
 [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 53.9 bits (128), Expect = 4e-06, Method: Compositional matrix adjust.
 Identities = 38/101 (37%), Positives = 54/101 (53%), Gaps = 3/101 (2%)

Query 42	ILMLLAEQISTNAKIAEKLKISPAAVTKALKLQEELIKSSRATN DERRVVLWLSTEKAV	101
	++ L E TNA+IAE L I P++VT +K+L+E E++ + ND+RV LTEK	
Sbjct 47	LVELWNEDGLTNAEIAELLDIKPSSVTTQVKQLEEAEMVIRKDENDKRVNRIFLTEKGR	106
Query 102	PVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTE	142
	+ T H T GN TDEEQE ++ + L E	
Sbjct 107	EAQETRDTMHNDISSETI--FGN-LTDEEQEQLANLMEKLVE	144

>ref|ZP_02617530.1| transcriptional regulator, MarR family [Clostridium botulinum Bf]
 gb|EDT85893.1| transcriptional regulator, MarR family [Clostridium botulinum Bf]
 Length=174

Score = 53.9 bits (128), Expect = 4e-06, Method: Compositional matrix adjust.
 Identities = 35/113 (30%), Positives = 62/113 (54%), Gaps = 2/113 (1%)

Query 30	ESDVVLTLSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKLQEELIKSSRATN	87
	++D+K S E H++ + + +S N IA+ L ++ + +K KL +++IK+ + N	
Sbjct 58	DNDIKGISLSEFHVICIGKNNMSNNIFIAKDLNMTKGGISKINSKLLSKDIIKADKIEN	117
Query 88	DERVVVLSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL	140
	D+R + +SLTEK + + K H HEK ++ + + EE I KFL L	
Sbjct 118	DKREIYYSLTEKGIALFKLHEHIHEKEREKLMKILSNYKLEEITTILKFLEDL	170

>ref|YP_861960.1| **G** MarR family transcriptional regulator [Gramella forsetii KT0803]
 emb|CAL66893.1| **G** MarR family transcriptional regulator protein [Gramella forsetii

KT0803]
Length=158

GENE ID: 4650237 GFO 1928 | MarR family transcriptional regulator
[Gramella forsetii KT0803] (10 or fewer PubMed links)
Score = 53.9 bits (128), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 39/112 (34%), Positives = 65/112 (58%), Gaps = 8/112 (7%)

Query 1 MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHIMLLAEQ--ISTNAKIAE 58
+ L NQI + ++ + ++ L K E LT Q +L++L E+ +S N K I E
Sbjct 7 LKLENQICFPPIYSVSRLLTAKPYLDKLE---LTYPQYLVLLVLWEEHKLSVN-KIGE 61
Query 59 KKLKISPAAVTKALKKLQEQLIKSSRATNDERVVWLWSLTEKAVPVAKEHATH 110
KL ++ ++ LK+++ EL+K +R++NDE VL LT+K + KE A H
Sbjct 62 KMLMNTNTLSPPLLKRMEKNELLKRNRSNSNDERTVLVGLTDKGLSY-KEKAHH 112

>ref|NP_391388.1| **G** hypothetical protein BSU35080 [Bacillus subtilis subsp. subtilis str. 168]
ref|ZP_03593305.1| hypothetical protein Bsubs1_18986 [Bacillus subtilis subsp. subtilis str. 168]
ref|ZP_03597590.1| hypothetical protein BsubsN3_18902 [Bacillus subtilis subsp. subtilis str. NCIB 3610]
6 more sequence titles
ref|ZP_03601994.1| hypothetical protein BsubsJ_18865 [Bacillus subtilis subsp. subtilis str. JH642]
ref|ZP_03606279.1| hypothetical protein BsubsS_19021 [Bacillus subtilis subsp. subtilis str. SMY]
sp|P40762.1|YVMB_BACSU RecName: Full=Uncharacterized HTH-type transcriptional regulator yvmb
emb|CAA85355.1| unnamed protein product [Bacillus subtilis]
gb|AAC67278.1| YzhA [Bacillus subtilis]
emb|CAB15513.1| **G** yvmb [Bacillus subtilis subsp. subtilis str. 168]
Length=169

GENE ID: 936625 vvmB | vvmB [Bacillus subtilis subsp. subtilis str. 168]
(10 or fewer PubMed links)

Score = 53.5 bits (127), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 36/91 (39%), Positives = 53/91 (58%), Gaps = 2/91 (2%)

Query 52 TNAKIAEKLKISPAAVTKALKKLQEQLIKSSRATNDERVVWLWSLTEKAVPVAKEH-ATH 110
NA IA K+ +S A VTK KL ++E I S + T++++ V + LT K + H H
Sbjct 63 NNAGIARKMNLSKANVTKISTKLKEEFINSYQLTDNKVEVFKLTRKGRRIFDLHEKLH 122
Query 111 HEKTLSTYQELGNKFTDEEQEVISKFLSALT 141
+K L+ YQ L + F+ EEQ+ + KFL LT
Sbjct 123 KKKELAFYQFL-DSFSQEEQKAVLKFLFQLT 152

>ref|ZP_02994615.1| hypothetical protein CLOspo_01734 [Clostridium sporogenes ATCC 15579]
gb|EDU38872.1| hypothetical protein CLOspo_01734 [Clostridium sporogenes ATCC 15579]
Length=174

Score = 53.5 bits (127), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 34/113 (30%), Positives = 63/113 (55%), Gaps = 2/113 (1%)

Query 30 ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQLIKSSRATN 87
++D+K S E H++ + + +S N IA++L ++ + +K KL +++IK+ + N
Sbjct 58 DNDIKEISLSEFHVICIGKNNMSNNFIAKELNMTKGGISKINSKLLSKDIIKADKIEN 117
Query 88 DERVVWLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
D+R + +SLTEK + + K H H+K ++ + + EE I KFL L
Sbjct 118 DKREIYYSLTEKGVLFKLHEYLHKKEQEKLMKILSNYKQEEITTILKFDDL 170

>ref|ZP_01994138.1| hypothetical protein DORLON_00120 [Dorea longicatena DSM 13814]
gb|EDM64274.1| hypothetical protein DORLON_00120 [Dorea longicatena DSM 13814]
Length=153

Score = 53.1 bits (126), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 36/111 (32%), Positives = 55/111 (49%), Gaps = 4/111 (3%)

Query 35 LTSTQEHIMLLAEQISTN-AKIAEKLKISPAAVTKALKKLQEQLIKSSRATNDERVV 93
LT+ H++ + N + IA KL I+ ++T A+ L + ++ R+ D RVVL
Sbjct 37 LTNNNDMHVIEAVGLGDGNMSSIARKLNITVGSLTTAMNSLVNKRYVERHRSEEDRRVVL 96
Query 94 WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
LTEK V H +H + Q + +K D E V+ K L AL+E F
Sbjct 97 VKLTEKGVKAYHHHEDYHRQMT---QAILDKLDDTELPVLVKTLDALSEFF 144

>ref|ZP_03294064.1| hypothetical protein CLOHIR_02015 [Clostridium hiranonis DSM 13275]
gb|EEA84316.1| hypothetical protein CLOHIR_02015 [Clostridium hiranonis DSM 13275]
Length=166

Score = 53.1 bits (126), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 37/131 (28%), Positives = 68/131 (51%), Gaps = 6/131 (4%)

Query 13 TIMQFAENKHEILLGKCESDVKLTSTQEHIMLLAEQISTN-AKIAEKLKISPAAVTKAL 71

Annex 1

Sbjct 20 T +F HE G+ K+ + H++ + E N +++++E+L I+ AV++ L 74
 TYYKFLSTPHEYYPG-----KMHMREVHVITEIGEGGLDNISELSERLNITKGAVSQYL 74
 Query 72 KKLQEQLIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSYQELGNKFTDDEQE 131
 KKL++I+ + D+R LTEK + K H + E+ + N+FT+EE E
 Sbjct 75 KKLEKKGFIERVQESEDKRQYSVRLTEKGKELDKIHTKYDEEQYAKACPFNEFTEEELE 134
 Query 132 VISKFISALTE 142
 +I +F + E
 Sbjct 135 LICRFEARFAE 145

>ref|ZP_02211326.1| hypothetical protein CLOBAR_00939 [Clostridium bartlettii DSM 16795]
 gb|EDQ97187.1| hypothetical protein CLOBAR_00939 [Clostridium bartlettii DSM 16795]
 Length=150

Score = 52.4 bits (124), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 33/94 (35%), Positives = 50/94 (53%), Gaps = 3/94 (3%)

Query 52 TNAKIAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWSLTEKAVPVAKEHATHH 111
 T +IA L+I+ +T A+ +L ++ + SR D RVV SLTEK K HA H
 Sbjct 53 TMGEIAHDLRITVGTLTSAINRLIKKGYAERSTEEDRRVVLVSLTEKGKHAYKIADFH 112
 Query 112 EKTLSTYQELGNKFTDDEQEVIISKFLSALTEEFQ 145
 ++ + Q N + DEEQEV+ + + F+
 Sbjct 113 KEMV---QATLNSYNDEEQEVLCDVIEKINIFFE 143

>ref|YP_001390364.1| **G** MarR family transcriptional regulator [Clostridium botulinum F str. Langeland]
 gb|ABS39442.1| **G** transcriptional regulator, MarR family [Clostridium botulinum F str. Langeland]
 Length=174

GENE ID: 5405444 CLI_1098 | MarR family transcriptional regulator
 [Clostridium botulinum F str. Langeland]

Score = 52.4 bits (124), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 34/113 (30%), Positives = 62/113 (54%), Gaps = 2/113 (1%)

Query 30 ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKLQEQLIKSSRATN 87
 ++D+K S E H++ + + + S N IA+L ++ + +K KL +++IK+ + N
 Sbjct 58 DNDIKGISLSEFHVICIGKNMSNNIFIAKELNMTKGGISKINSKLLSKDIKADKIEN 117
 Query 88 DERVVVLWSLTEKAVPVAKEHATHHEKTLSYQELGNKFTDDEQEVIISKFLSAL 140
 D+R + +SLTEK + + K H HEK ++ + + EE I FL L
 Sbjct 118 DKREIYYSLTEKGIALFKLHEHLHEKERELKMKILSNYKLEEITILNFLEDL 170

>ref|YP_001786407.1| **G** MarR family transcriptional regulator [Clostridium botulinum A3 str. Loch Maree]
 gb|ACA55750.1| **G** transcriptional regulator, MarR family [Clostridium botulinum A3 str. Loch Maree]
 Length=174

GENE ID: 6154364 CLK_0459 | MarR family transcriptional regulator
 [Clostridium botulinum A3 str. Loch Maree] (10 or fewer PubMed links)

Score = 51.6 bits (122), Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 33/113 (29%), Positives = 62/113 (54%), Gaps = 2/113 (1%)

Query 30 ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKLQEQLIKSSRATN 87
 ++D+K S E H++ + + + N IA+L ++ + +K KL +++IK+ + N
 Sbjct 58 DNDIKGISLSEFHVICIGKNMPNNIFIAKELNMTKGGISKINSKLLSKDIIRADKIEN 117
 Query 88 DERVVVLWSLTEKAVPVAKEHATHHEKTLSYQELGNKFTDDEQEVIISKFLSAL 140
 D+R + +SLTEK + + K H HEK ++ + + EE I KFL L
 Sbjct 118 DKREIYYSLTEKGIALFKLHEHLHEKERELKMKILSNYKQEEITILKFLEDL 170

>ref|YP_808725.1| **G** transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
 gb|ABJ72303.1| **G** Transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
 Length=292

GENE ID: 4432217 LACR_0742 | transcriptional regulator
 [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 51.2 bits (121), Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 35/91 (38%), Positives = 50/91 (54%), Gaps = 3/91 (3%)

Query 52 TNAKIAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWSLTEKAVPVAKEHATHH 111
 TNA+IAE L I P+VT +K+L+E E++ + ND+RV LTEK + T H
 Sbjct 57 TNAEIAELLDIKPSSVTAQVKOLEEAEMVIRKDENDKRVNRIFLTEKGREAQETRDTMH 116
 Query 112 EKTLSTYQELGNKFTDDEQEVIISKFLSALTE 142
 T GN TDEEQ+ ++ + L E
 Sbjct 117 NDISETI--FGN-LTDEEQKQLANLMEKLVE 144

Annex 1

>ref|YP_001698248.1| **G** MarR family transcriptional regulator [Lysinibacillus sphaericus C3-41]
 gb|AC40118.1| **G** transcriptional regulator, MarR family [Lysinibacillus sphaericus C3-41]
 Length=162

GENE ID: 6022244 BspH 2567 | MarR family transcriptional regulator
 [Lysinibacillus sphaericus C3-41] (10 or fewer PubMed links)

Score = 51.2 bits (121), Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 36/111 (32%), Positives = 60/111 (54%), Gaps = 1/111 (0%)

Query 36	TSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLW	94
	T TQ HI+ + Q S N ++E L +S A+TKA+KK+ E+ +I +R +++ V +	
Sbjct 44	TLTQLHIVSAIKAQGSANNTFLSETLNVS KPAITKAIKKMLEKNVIVETRQEANQKEVHY	103
Query 95	SLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ	145
	LT ++ H HEK + Y L + F +E E I FL +T++ +	
Sbjct 104	LLTAFGKQLSSIHEQLHEKARNRYLRLDSFNTDELETIVTFLEMIDDKLK	154

>ref|NP_266864.1| **G** transcription regulator [Lactococcus lactis subsp. lactis II1403]
 gb|AAK04806.1|AE006304_6 **G** transcription regulator [Lactococcus lactis subsp. lactis II1403]
 Length=291

GENE ID: 1114333 rmaB | transcription regulator
 [Lactococcus lactis subsp. lactis II1403] (10 or fewer PubMed links)

Score = 51.2 bits (121), Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 35/91 (38%), Positives = 50/91 (54%), Gaps = 3/91 (3%)

Query 52	TNAKIAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWSLTEKAVPVAKEHATHH	111
	TNA+IAE L I P++VT +K+L+E E++ + ND+RV LT+K + T H	
Sbjct 57	TNAEIAELLDIKPSSVTAQVKQLEEAEMVIRKQDENDKRVSRIFLTDKGREAQETRDTMH	116
Query 112	EKTLS TQELGNKFTDEEQEVISKFLSALTE	142
	T GN TDEEQE ++ + L E	
Sbjct 117	NDISETI--FGN-LTDEEQEQLAFLMEKLVE	144

>ref|ZP_01723095.1| transcriptional regulator, MarR family protein [Bacillus sp. B14905]
 gb|EAZ86562.1| transcriptional regulator, MarR family protein [Bacillus sp. B14905]
 Length=162

Score = 50.4 bits (119), Expect = 4e-05, Method: Compositional matrix adjust.
 Identities = 35/111 (31%), Positives = 60/111 (54%), Gaps = 1/111 (0%)

Query 36	TSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLW	94
	T TQ HI+ + Q S N ++E L +S A+TKA+KK+ E+ +I +R +++ + +	
Sbjct 44	TLTQLHIVSAIKAQGSANNTFLSETLNVS KPAITKAIKKMLEKNVIVETRQEANQKEIHY	103
Query 95	SLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ	145
	LT ++ H HEK + Y L + F +E E I FL +T++ +	
Sbjct 104	LLTAFGKQLSSIHEQLHEKARNRYLRLDSFNTDELETIVTFLEMIDDKLK	154

>ref|YP_808147.1| **G** transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
 gb|ABJ71725.1| **G** Transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
 Length=169

GENE ID: 4432499 LACR_0099 | transcriptional regulator
 [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 50.4 bits (119), Expect = 5e-05, Method: Compositional matrix adjust.
 Identities = 27/98 (27%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

Query 41	HILMLLAEQISTNAKIAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWSLTEKA	100
	HIL L ++ T ++A KL ++ VT+A++ L + + + + +A ND++ + + +T K	
Sbjct 53	HILSALTKKDLTGIELATKLSVTGGVTRAVONLIKHQFLTTYQADNDKKKIYYHITTKG	112
Query 101	VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS	138
	+ VA H H+ ++ +K+ + E+ +I FLS	
Sbjct 113	LKVASIHDKMHKIMDLKLGQIFDKYNENEKSIILNFLS	150

>ref|NP_786298.1| **G** transcription regulator [Lactobacillus plantarum WCFS1]
 emb|CAD65154.1| **G** transcription regulator [Lactobacillus plantarum WCFS1]
 Length=178

GENE ID: 1063436 lp_2967 | transcription regulator
 [Lactobacillus plantarum WCFS1] (10 or fewer PubMed links)

Score = 50.1 bits (118), Expect = 6e-05, Method: Compositional matrix adjust.
 Identities = 33/104 (31%), Positives = 57/104 (54%), Gaps = 5/104 (4%)

Query 39	QEHILMLLAEQIS--TNAKIAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWSL	96
	Q IL +LA+ + TNA+IAE L I P++V+ L +L++ LI+ + +D+RVV+ L	
Sbjct 43	QMGILRVLADAPAGLNTNAEIAEILDIRPSSVSATLNRLEDGGGLIEREPASAHDKRIVVRL	102

Query 97 TEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
 +++ +A A + T +L TD+E+ + L L
 Sbjct 103 SDRGREMAHDRA---QGTSDLADQLFGNLTDERNQLOHLLDKL 143

>ref|YP_757477.1| **G** MarR family transcriptional regulator [Maricaulis maris MCS10]
 gb|ABI66539.1| **G** transcriptional regulator, MarR family [Maricaulis maris MCS10]
 Length=143

GENE ID: 4285355 Mmar10_2247 | MarR family transcriptional regulator
 [Maricaulis maris MCS10]

Score = 50.1 bits (118), Expect = 6e-05, Method: Compositional matrix adjust.
 Identities = 39/146 (26%), Positives = 75/146 (51%), Gaps = 5/146 (3%)

Query 1 MSLANQIDQFLGTTIMQFAENK-HEILLGKCESDVKLTSTQEHLMLLAEQISTN-AKIAE 58
 M+ A +D+ L +++ A K+ +S +TS Q +L LLA + I E
 Sbjct 1 MARARAVDRRLFLLLEIAARKLNRDADARLKSVAGVTSAQAAVLFLARRGERRMGDIGE 60

Query 59 KLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWLSTEKAVPVAKEHATHHEKTLSTY 118
 L + P AVT + +++ L+ + +D+R + SLTEK + + A H + L+T
 Sbjct 61 MLSLHPAPPATGLVNRMEALGLVTKKTPSDKRSIAVSLTEKGRALG-DTADHILRDLNT- 118

Query 119 QELGNKFTDEEQEVISKFLSALTEEF 144
 EL N+ +E+ +++ + L+ + +F
 Sbjct 119 -ELENRLGEEDADMLHRLVTRIAVDF 143

>ref|NP_391385.1| **G** hypothetical protein BSU35050 [Bacillus subtilis subsp. subtilis
 str. 168]
 ref|ZP_03593302.1| hypothetical protein Bsubs1_18971 [Bacillus subtilis subsp. subtilis
 str. 168]
 ref|ZP_03597587.1| hypothetical protein BsubsN3_18887 [Bacillus subtilis subsp.
 subtilis str. NCIB 3610]
 ref|ZP_03601991.1| hypothetical protein BsubsJ_18850 [Bacillus subtilis subsp. subtilis
 str. JH642]
 ref|ZP_03606276.1| hypothetical protein BsubsS_19006 [Bacillus subtilis subsp. subtilis
 str. SMY]
 sp|O34692.1| YVNA_BACSU RecName: Full=Uncharacterized HTH-type transcriptional regulator
 yvnA
 gb|AAC67281.1| YvnA [Bacillus subtilis]
 emb|CAB15510.1| **G** yvnA [Bacillus subtilis subsp. subtilis str. 168]
 Length=157

GENE ID: 936639 vvnA | vvnA [Bacillus subtilis subsp. subtilis str. 168]
 (10 or fewer PubMed links)

Score = 50.1 bits (118), Expect = 6e-05, Method: Compositional matrix adjust.
 Identities = 30/104 (28%), Positives = 59/104 (56%), Gaps = 1/104 (0%)

Query 36 TSTQEHLMLL-AEQISTNAKIAEKLKISPAAVTKALKLQEQELIKSSRATNDERVVLW 94
 T TQ HI+ + Q N+ +A +L IS AAV+KA+ L + +I ++ +++ +
 Sbjct 48 TLTQLHIVSCIHTSQNVNNNSFLASRHLHISKAQSKAVHALLKHNIITVTKKPGNKKEIFY 107

Query 95 SLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS 138
 +LT+ +A H HEK Y++L N+F+ ++ + ++ F +
 Sbjct 108 TLTDSGRKLAALHEQLHEKAKEQYKQLFNEFSIDDLKTVTAFFN 151

>ref|NP_111681.1| **G** transcription regulator (SlyA-related) [Thermoplasma volcanium
 GSS1]
 dbj|BAB60329.1| **G** hypothetical protein [Thermoplasma volcanium GSS1]
 Length=143

GENE ID: 1441302 TVN1162 | transcription regulator (SlyA-related)
 [Thermoplasma volcanium GSS1] (10 or fewer PubMed links)

Score = 49.7 bits (117), Expect = 7e-05, Method: Compositional matrix adjust.
 Identities = 30/81 (37%), Positives = 45/81 (55%), Gaps = 0/81 (0%)

Query 26 LGKCESDVKLTSTQEHLMLLAEQISTNAKIAEKLKISPAAVTKALKLQEQELIKSSRA 85
 +G+ S + + IL LL+E ST K+AE ++PA +T L +++ Q LI SR+
 Sbjct 27 MGESLSHISAKPIEVRLYLLSEDESTVNKLAELTDVTPAWITGTLDEMESQGLIVRSRS 86

Query 86 TNDERVVLWLSLTEKAVPVAKE 106
 D RVV +TEK + V E
 Sbjct 87 GEDRRVVNVNWHITEKGIEVLNE 107

>ref|NP_419215.1| **G** MarR family transcriptional regulator [Caulobacter crescentus
 CB15]
 ref|YP_002515775.1| **G** transcriptional regulator, MarR family [Caulobacter crescentus
 NA1000]
 gb|AAK22383.1| **G** transcriptional regulator, MarR family [Caulobacter crescentus
 CB15]
 gb|ACL93867.1| **G** transcriptional regulator, MarR family [Caulobacter crescentus
 NA1000]
 Length=147

GENE ID: 942105 CC_0396 | MarR family transcriptional regulator
 [Caulobacter crescentus CB15] (10 or fewer PubMed links)

Score = 49.3 bits (116), Expect = 9e-05, Method: Compositional matrix adjust.
 Identities = 32/119 (26%), Positives = 63/119 (52%), Gaps = 4/119 (3%)

Query 27	GKCESDVKLSTQEHILMLLAEQIST-NAKIAEKLKISPAAVTKALKLQEQLIKSSRA	85
	G+ ++ LT+ Q +L L E+ + + A +L ++P+A+T + ++ EL++	
Sbjct 26	GRMAAEGGLTAAQSGVLFGERDLAGILEAADALDLAPSAMTGLIDRMARAEVERRAD	85
Query 86	TNDERVVLWLSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF	144
	D R + LT+K A++ A + ++ +L FTDEE V+S++L++L +F	
Sbjct 86	AKDGRAMHLHLDKGR-AARDTAKAGLRGVNA--QLTEGFTDEEISVVSRWLASLQTKF	141

>ref|YP_001031482.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]

gb|CAL96727.1| **G** transcriptional regulator, MarR family [Lactococcus lactis subsp. cremoris MG1363]
 Length=172

GENE ID: 4798609 rmaD | MarR family transcriptional regulator
 [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 49.3 bits (116), Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 26/98 (26%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

Query 41	HILMLLAEQISTNAKIAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWLSLTEKA	100
	HIL L ++ T ++A KL ++ VT+A++ L + + + + A ND++ + + +T K	
Sbjct 56	HILSALTKKDLTGIELATKLSVTRGGVTRAVQNLIKHQFLTTYQADNDKKKIYYHITTKG	115
Query 101	VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS	138
	+ VA H H+ ++ +K+ + ++ +I FLS	
Sbjct 116	LKVASIHDKMHKIMDLKLGQIFDKYNENDKSIILNFLS	153

>ref|NP_603578.1| **G** MarR family transcriptional regulator [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]

gb|AAL94877.1| **G** Transcriptional regulator, MarR family [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]
 Length=225

GENE ID: 991648 FN0681 | MarR family transcriptional regulator
 [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] (10 or fewer PubMed links)

Score = 48.9 bits (115), Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 29/88 (32%), Positives = 50/88 (56%), Gaps = 3/88 (3%)

Query 35	LTSTQEHILMLLAE-QISTNAKIAEKLKISPAAVTKALKLQEQLIKSSRATNDERVV	92
	LT T+ HI+ + E Q++ N ++A+K+ I+ T A+ KL ++ I +R+T D R V	
Sbjct 34	LTHTELHIIIESIGENTQLTMN-ELADKIGITMGTATVAISKLSDKGYIDRARSTTDRRKV	92
Query 93	LWSLTEKAVPVAKEHATHHEKTLSTYQE	120
	SLT+K V H H+ ++ E	
Sbjct 93	FVSLTKKGVDALTYHNNYHKMIMASITE	120

>ref|YP_138915.1| **G** MarR family transcriptional regulator [Streptococcus thermophilus LMG 18311]

gb|AAV60100.1| **G** transcriptional regulator, MarR family [Streptococcus thermophilus LMG 18311]
 Length=144

GENE ID: 3164787 stu0381 | MarR family transcriptional regulator
 [Streptococcus thermophilus LMG 18311] (10 or fewer PubMed links)

Score = 48.9 bits (115), Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 31/90 (34%), Positives = 51/90 (56%), Gaps = 3/90 (3%)

Query 51	STNAKIAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWLSLTEKAVPVAKEHATH	110
	+T + +A +L ++ VT +L KL+++ I +R++ D RVV SL++K V + H	
Sbjct 50	TPPSAVAREMLMTLGTVTTSLNKLEKKGYIIRTRSSVDRRVVHLSLSKKGRLVYRLHRGF	109
Query 111	HEKTLSTYQELGNKFTDEEQEVISKFLSAL	140
	H+ + T E F DEE +V+SK L L	
Sbjct 110	HKSMVKTITE---GFNDEELKVMMSKGLENL	136

>ref|YP_002165566.1| **G** possible MarR family transcriptional regulator [Fusobacterium nucleatum subsp. polymorphum ATCC 10953]

gb|EDK89119.1| **G** possible MarR family transcriptional regulator [Fusobacterium nucleatum subsp. polymorphum ATCC 10953]
 Length=225

GENE ID: 6818656 FNP_1336 | possible MarR family transcriptional regulator
 [Fusobacterium nucleatum subsp. polymorphum ATCC 10953]

Score = 48.9 bits (115), Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 29/88 (32%), Positives = 50/88 (56%), Gaps = 3/88 (3%)

Query 35	LTSTQEHILMLLAE-QISTNAKIAEKLKISPAAVTKALKLQEQLIKSSRATNDERVV	92
	LT T+ HI+ + E Q++ N ++A+K+ I+ T A+ KL ++ I +R+T D R V	
Sbjct 34	LTHTELHIIIESIGENTQLTMN-ELADKIGITMGTATVAISKLSDKGYIDRARSTTDRRKV	92
Query 93	LWSLTEKAVPVAKEHATHHEKTLSTYQE	120
	SLT+K V H H+ ++ E	

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Sbjct 93 FVSLTKKGVDALTYHNNYHKMIMASITE 120·

>ref|ZP_00144611.1| Transcriptional regulator, MarR family [Fusobacterium nucleatum subsp. *Vincentii* ATCC 49256]
 gb|EAA23791.1| Transcriptional regulator, MarR family [Fusobacterium nucleatum subsp. *Vincentii* ATCC 49256]
 Length=225

Score = 48.9 bits (115), Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 29/88 (32%), Positives = 50/88 (56%), Gaps = 3/88 (3%)

Query 35 LTSTQEHILMLLAE--QISTNAKIAEKLKISPAAVTKALKLQEQUELIKSSRATNDERRVV 92
 LT T+ HI+ + E Q++ N ++A+K+ I+ T A+ KL ++ I +R+T D R V

Sbjct 34 LTHTELHIESIGENTQLTMN-ELADKIGITMGATVAISKLSDKGYIDRARSTTDRRKV 92

Query 93 LWSLTEKEAVPVAKEAVHATHHEKTILSTYQE 120
 SLT+K V H +H+ +++ E

Sbjct 93 FVSLTKKGVDALTYHNNYHKMIMASITE 120

>ref|YP_819912.1| **G** MarR family transcriptional regulator [Streptococcus thermophilus LMD-9]
 gb|ABJ65716.1| **G** transcriptional regulator, MarR family [Streptococcus thermophilus LMD-9]

Length=144

GENE ID: 4437359 **STER_0428** | MarR family transcriptional regulator
 [Streptococcus thermophilus LMD-9] (10 or fewer PubMed links)

Score = 48.9 bits (115), Expect = 1e-04, Method: Compositional matrix adjust.
 Identities = 31/90 (34%), Positives = 51/90 (56%), Gaps = 3/90 (3%)

Query 51 STNAKIAEKLKISPAAVTKALKLQEQUELIKSSRATNDERRVWLWSLTEKEAVPVAKEAVHATH 110
 +T + +A +L ++ VT +L KL+++ I +R++ D RVV SL++K V + H

Sbjct 50 TPPSAVAREMLMLTGTVTTSNLKLEKKGYIIRTRSSVDRVVHLSLSKKGRLVYRLHRAF 109

Query 111 HEKTILSTYQELGNKFTDEEQEVISKFLSAL 140
 H+ + T E F DEE +V+SK L L

Sbjct 110 HKSMVKITTE---GFNDEELKVMSKGLENL 136

>ref|YP_079349.1| **G** transcriptional regulator YvmB [Bacillus licheniformis ATCC 14580]

gb|AAU23711.1| **G** possible transcriptional regulator YvmB [Bacillus licheniformis ATCC 14580]

Length=161

GENE ID: 3031484 **yvmB** | transcriptional regulator YvmB
 [Bacillus licheniformis ATCC 14580] (10 or fewer PubMed links)

Score = 48.5 bits (114), Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 35/117 (29%), Positives = 59/117 (50%), Gaps = 4/117 (3%)

Query 29 CESDVKL---TSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKLQEQUELIKSSR 84
 ESDVK T H++ + ++ N IA+K+ +S A +T K KL ++ LIK +

Sbjct 36 AESDVKRPGNMTTIVISCGHDEPINNTGIAKKMNLSKANITKISSKLLKEGLIKRFO 95

Query 85 ATNDERRVVLWLSLTEKEAVPVAKEAVHATHHEKTILSTYQELGNKFTDEEQEVISKFLSALT 141

T++++ + + LT V + H H++ + + F+ EQ I KFL LT

Sbjct 96 LTDNKKEIYFRLTPSGKQVFELHEKLHQHQKADQFSRFLDSFSTAEGQAILKFLQGLT 152

>ref|ZP_01219563.1| putative transcriptional regulator, MarR family protein [Photobacterium profundum 3TCK]

gb|EAS43796.1| putative transcriptional regulator, MarR family protein [Photobacterium profundum 3TCK]

Length=138

Score = 48.1 bits (113), Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 39/143 (27%), Positives = 73/143 (51%), Gaps = 13/143 (9%)

Query 7 IDOFLGTIMQFAEN---KHEILLGKCESDVKLTSTQEHILMLLAEQISTNAK-IAEKLK 61
 I+O TI++F E + ++ GK + Q HI+ +L + K +A+K+

Sbjct 4 IEQLNHTIIEFYEKLSSWEQSUVVRGKG----FSLPQVHIVEILGAHGMARMKELADKIG 58

Query 62 ISPAAVTKALKLQEQUELIKSSRATNDERRVVLWLSLTEKEAVPVAKEAVHATHHEKTILSTYQEL 121

++ +T + K+ + ELI+ +D R +L LTEK V + +EH H LS Q++

Sbjct 59 VTTGTLTVQVDKVMQAELIQRRPHESDRRSILVLDTEKGVEMYQEHDHLH---LSLTQDI 115

Query 122 GNKFTDEEQEVISKFLSALTEEF 144

+ D E++ + +L+ + +EF

Sbjct 116 TAQLDDVERKNLLMYLTKMNQEF 138

>ref|YP_091766.1| **G** YvmB [Bacillus licheniformis ATCC 14580]

gb|AAU41073.1| **G** YvmB [Bacillus licheniformis DSM 13]

Length=163

GENE ID: 3097946 **vvmB** | YvmB [Bacillus licheniformis ATCC 14580]

(10 or fewer PubMed links)

Score = 48.1 bits (113), Expect = 2e-04, Method: Compositional matrix adjust.

Identities = 35/117 (29%), Positives = 59/117 (50%), Gaps = 4/117 (3%)

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Query 29 CESDVKL---TSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKLQEELIKSSR 84
 Sbjct 38 ESDVK T H++ + ++ N IA+K+ +S A +TK KL ++ LIK +
 Query 85 ATNDERVVLWSLTEKAVPVAKEHATHHEKTLSYQELGNKFTDEEQEVISKFLSALT 141
 Sbjct 98 LTDNKKEIYFRLTPSGKQVFELHEKLHQHQKADQFSRFLDSFSTAEGQAILKFLQGLT 154

>ref|YP_129221.1| **G** MarR family transcriptional regulator [Photobacterium profundum SS9]

emb|CAG19419.1| **G** putative transcriptional regulator, MarR family [Photobacterium profundum SS9]
 Length=138

GENE ID: 3122954 PBPRA1008 | MarR family transcriptional regulator [Photobacterium profundum SS9] (10 or fewer PubMed links)

Score = 48.1 bits (113), Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 39/143 (27%), Positives = 73/143 (51%), Gaps = 13/143 (9%)

Query 7 IDQFLGTMQFAEN---KHEILLGKCESDVKLTSTQEHILMLLAEQISTNAK-IAEKLK 61
 Sbjct 4 I+Q TI++F E + ++ GK + Q HI+ +L + K +A+K+
 IEQLNHTIIIEFYKEKLSWEQSNSVVRKGK-----FSLPQIHHIVEILGAHGMARMKELADKIG 58

Query 62 ISPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSYQEL 121
 Sbjct 59 VTTGTLLTVQVDKVMQAELIQRRPHESDRRSILVLDLTEQGVEMYQEHDHHL---LSLTQDI 115
 ++ +T + K+ + ELI+ +D R +L LTE+ V + +EH H LS Q++

Query 122 GNKFTDEEQEVISKFLSALTEEF 144
 Sbjct 116 TAKLDDTERKNNLMLYLTKMNQEF 138
 K D E++ + +L+ + +EE

>ref|ZP_00990845.1| hypothetical transcriptional regulator, MarR family [Vibrio splendidus 12B01]
 gb|EAP94213.1| hypothetical transcriptional regulator, MarR family [Vibrio splendidus 12B01]
 Length=301

Score = 48.1 bits (113), Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 35/117 (29%), Positives = 62/117 (52%), Gaps = 1/117 (0%)

Query 25 LLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKLQEELIKSSR 84
 Sbjct 19 +L K D+ L Q H L+ L +Q T +A+KL I + ++A+ L + LI++S
 MLDKDCGDIALPPIQAHTLIELEQQPLTVNQLADKLNIDKSNSARAVNNLAKNSLIQTSP 78

Query 85 ATNDERVVLWSLTEKAV-PVAKEHATHHEKTLSYQELGNKFTDEEQEVISKFLSAL 140
 Sbjct 79 ND+R V+ S+TE+ +A+ H+ ++ S + L T + I +L AL
 HPNDKRSVVVASVTEQGIKTLAQHLSQQNFYDSVLERLTEAQVSGGIKHYLKAL 135

>ref|YP_001319891.1| **G** MarR family transcriptional regulator [Alkaliphilus metallireducens QYMF]

gb|ABR48232.1| **G** transcriptional regulator, MarR family [Alkaliphilus metallireducens QYMF]
 Length=143

GENE ID: 5312143 Amet_2072 | MarR family transcriptional regulator [Alkaliphilus metallireducens QYMF]

Score = 47.8 bits (112), Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 27/67 (40%), Positives = 42/67 (62%), Gaps = 1/67 (1%)

Query 35 LTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKLQEELIKSSRATNDERVVL 93
 Sbjct 37 +T TQ L++L E+ AK + EKL + +T LKKL+ +ELI R+T DER+++
 ITYTQYITLLVWEPKPKITAKEGEKLYLDSGTLTPLKKLESKELITRKRSTKDERIMI 96

Query 94 WSLTEKA 100
 Sbjct 97 VTLTDKG 103
 +LT+K

>ref|YP_001838202.1| **G** MarR family transcriptional regulator [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)']

gb|ABZ96926.1| **G** Putative transcriptional regulator, MarR family [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)']
 Length=133

GENE ID: 6222463 LEPBI_I0798 | MarR family transcriptional regulator [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)'] (10 or fewer PubMed links)

Score = 47.8 bits (112), Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 26/71 (36%), Positives = 45/71 (63%), Gaps = 1/71 (1%)

Query 31 SDVKLTSTQEHILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKLQEELIKSSRATNDE 89
 Sbjct 26 +D+ LT Q +++++ E+ IST +KI +KL++ +T LK+L++ EL+ R NDE
 ADLGLTYPQYLVMVMWEEKISTVSKIGDKLQLDSGTLTPLKRLEQMELLDRMRNPND 85

Query 90 RVVLWSLTEKA 100
 Sbjct 86 RSVNIVLSKKKG 96
 R V L++K

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>ref|YP_108512.1| putative transcriptional regulatory protein [Burkholderia pseudomallei K96243]
 ref|YP_102754.1| MarR family transcriptional regulator [Burkholderia mallei ATCC 23344]
 ref|ZP_00438156.1| COG1846: Transcriptional regulators [Burkholderia mallei GB8 horse 4]
 46 more sequence titles

ref|YP_333321.1| MarR family transcriptional regulator [Burkholderia pseudomallei 1710b]
 ref|YP_992831.1| MarR family transcriptional regulator [Burkholderia mallei SAVP1]
 ref|YP_001026174.1| MarR family transcriptional regulator [Burkholderia mallei NCTC 10229]
 ref|YP_001058785.1| MarR family transcriptional regulator [Burkholderia pseudomallei 668]
 ref|YP_001080556.1| MarR family transcriptional regulator [Burkholderia mallei NCTC 10247]
 ref|YP_001066038.1| MarR family transcriptional regulator [Burkholderia pseudomallei 1106a]
 ref|ZP_01769009.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 305]
 ref|ZP_02102319.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 1106b]
 ref|ZP_02109049.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 1710a]
 ref|ZP_02266811.1| transcriptional regulator, MarR family protein [Burkholderia mallei FRL-20]
 ref|ZP_02403045.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei DM98]
 ref|ZP_02411585.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 14]
 ref|ZP_02447714.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 91]
 ref|ZP_02455880.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 9]
 ref|ZP_02471448.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei B7210]
 ref|ZP_02481920.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 7894]
 ref|ZP_02490126.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei NCTC 13177]
 ref|ZP_02498250.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 112]
 ref|ZP_02506273.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei BCC215]
 ref|YP_002009903.1| transcriptional regulator, MarR family [Burkholderia mallei ATCC 10399]
 ref|YP_002036065.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 1655]
 ref|YP_002022669.1| transcriptional regulator, MarR family [Burkholderia pseudomallei Pasteur 52237]
 ref|YP_002050288.1| transcriptional regulator, MarR family [Burkholderia pseudomallei S13]
 ref|YP_002060819.1| transcriptional regulator, MarR family [Burkholderia mallei FMH]
 ref|YP_002064980.1| transcriptional regulator, MarR family [Burkholderia mallei JHU]
 ref|YP_002106328.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 406e]
 ref|YP_002110157.1| transcriptional regulator, MarR family [Burkholderia mallei 2002721280]
 ref|ZP_03454874.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 576]
 emb|CAH35912.1| putative transcriptional regulatory protein [Burkholderia pseudomallei K96243]
 gb|AAU48847.1| transcriptional regulator, MarR family [Burkholderia mallei ATCC 23344]
 gb|ABA50381.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 1710b]
 gb|ABM52457.1| transcriptional regulator, MarR family [Burkholderia mallei SAVP1]
 gb|ABN02741.1| transcriptional regulator, MarR family [Burkholderia mallei NCTC 10229]
 gb|ABN82036.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 668]
 gb|ABN89050.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 1106a]
 gb|ABO05799.1| transcriptional regulator, MarR family [Burkholderia mallei NCTC 10247]
 gb|EBA46431.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 305]
 gb|EDK56373.1| transcriptional regulator, MarR family [Burkholderia mallei FMH]
 gb|EDK60534.1| transcriptional regulator, MarR family [Burkholderia mallei JHU]
 gb|EDK85546.1| transcriptional regulator, MarR family [Burkholderia mallei 2002721280]
 gb|EDO84870.1| transcriptional regulator, MarR family [Burkholderia pseudomallei

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gb|EDO91962.1| **G** transcriptional regulator, MarR family [Burkholderia pseudomallei Pasteur 52237]
 gb|EDP89187.1| **G** transcriptional regulator, MarR family [Burkholderia mallei ATCC 10399]
 gb|EDS86631.1| **G** transcriptional regulator, MarR family [Burkholderia pseudomallei S13]
 gb|EDU07559.1| **G** transcriptional regulator, MarR family [Burkholderia pseudomallei 1655]
 gb|EEC33252.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 576]
 Length=165

GENE ID: 3092472 BPSL1912 | putative transcriptional regulatory protein
 [Burkholderia pseudomallei K96243] (10 or fewer PubMed links)

Score = 47.4 bits (111), Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 33/126 (26%), Positives = 69/126 (54%), Gaps = 5/126 (3%)

Query 6	QIDQFLGTIMQFAEN-KHEILLGKCESDVKLTSTQEHIMLLA-EQISTNAKIAEKLKIS	63
Sbjct 17	QI+ +G +M + + ++ + +++++ +T TQ +L +LA + ST A++A + I	76
Query 64	PAAVTALKKKLQEQUELIKSSRATNDERVVLSLTEKAVPVAKEHATHHEKTLS	123
Sbjct 77	QINDSGVGLMSRVKSLMTNMTQRTQTELGITGTQATMLFMLAVGKCSTAAELAREY	133
Query 124	KFTDEE 129	
Sbjct 134	FT EE	
	GFTPEE 139	

>ref|YP_001961880.1| **G** Transcriptional regulator, marR family [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)']
 gb|ABZ93302.1| **G** Transcriptional regulator, marR family [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)']
 Length=145

GENE ID: 6388419 LBF_0770 | Transcriptional regulator, marR family
 [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)']
 (10 or fewer PubMed links)

Score = 47.4 bits (111), Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 26/71 (36%), Positives = 45/71 (63%), Gaps = 1/71 (1%)

Query 31	SDVKLTSTQEHIMLLL-AEQISTNAKIAEKLKISPAAVTKALKKLQEQUELIKSSRATNDE	89
Sbjct 38	+D+ LT Q +++++ E+IST +KI +KL++ +T LK+L++ EL+ R NDE	
	ADLGLTYPQYLVMVLWEEKISTVSKIGDKLQLDSGTLTPLLRLEQMELLDRMRNPNDE	97
Query 90	RVVLSLTEKA 100	
Sbjct 98	R V L++K	
	RSVNIVLSKKG 108	

>ref|YP_001310724.1| **G** MarR family transcriptional regulator [Clostridium beijerinckii NCIMB 8052]
 gb|ABR35768.1| **G** transcriptional regulator, MarR family [Clostridium beijerinckii NCIMB 8052]
 Length=155

GENE ID: 5294814 Cbei_3649 | MarR family transcriptional regulator
 [Clostridium beijerinckii NCIMB 8052]

Score = 47.4 bits (111), Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 30/109 (27%), Positives = 57/109 (52%), Gaps = 1/109 (0%)

Query 34	KLTSTQEHIMLLLAEQISTN-AKIAEKLKISPAAVTKALKKLQEQUELIKSSRATNDERRV	92
Sbjct 28	KLTFSQIHCIAAIYEYIEDANITKLSQELGMTTGAITKMCKKLLNEGYVSKYQKEGNNEKV	87
Query 93	LWSLTEKAVPVAKEHATHHEKTLS	141
Sbjct 88	QELGNKFTDEEQEVISKFLSALT + LTE + V + H HEK+ + +++ ++ DEE+ I KFL +	
	YYDLTEGLNVCEIHNRIHEKSYNKKDIIAQYNDEEKATILKFLHDMN 136	

>ref|ZP_01065868.1| hypothetical transcriptional regulator, MarR family protein [Vibrio sp. MED222]
 gb|EAQ52745.1| hypothetical transcriptional regulator, MarR family protein [Vibrio sp. MED222]
 Length=301

Score = 47.0 bits (110), Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 26/77 (33%), Positives = 45/77 (58%), Gaps = 0/77 (0%)

Query 25	LLGKCESDVKLTSTQEHIMLLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQUELIKSSR	84
Sbjct 19	+L K D+ L Q H L+ L +Q T ++A+KL I + ++A+ L + LI++S	
	MLDKDCGDIALPPIQAHTLIEQQPLTVNQLADKLNIDKSNASRAVNNLAKNSLIQTSP	78
Query 85	ATNDERVVLSLTEKAV 101	
Sbjct 79	ND+R V+ S+TE+ +	
	HPNDKRSVVASVTEQGI 95	

>ref|YP_140799.1| **G** MarR family transcriptional regulator [Streptococcus thermophilus CNRZ1066]

gb|AAV61984.1| **G** transcriptional regulator, MarR family [Streptococcus thermophilus CNRZ1066]
Length=144

GENE ID: 3167129 str0381 | MarR family transcriptional regulator
[Streptococcus thermophilus CNRZ1066] (10 or fewer PubMed links)

Score = 47.0 bits (110), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 30/90 (33%), Positives = 50/90 (55%), Gaps = 3/90 (3%)

Query 51 STNAKIAEKLKISPAAVTKALKLQEQUELIKSSRATNDERVVLWSLTEKAVPVAKEHATH 110
+T + +A +L ++ VT +L KL+++ I +R++ D RVV SL++K V + H
Sbjct 50 TTPSAVAREMLTLLGTVTTSLNKLEKKGYIIRTRSSVDRRRVHLSLSKKGRLVYRLHRGF 109

Query 111 HEKTLSPTYQELGNKFTDEEQEVISKFLSAL 140
H+ S + F DEE +V+SK L L
Sbjct 110 HK---SMVMRITERGFNDEELKVMMSKGLENL 136

>ref|YP_143999.1| **G** MarR family transcriptional regulator [Thermus thermophilus HB8]
gb|BAD70556.1| **G** transcriptional regulator MarR family [Thermus thermophilus HB8]
Length=144

GENE ID: 3168756 TTHA0733 | MarR family transcriptional regulator
[Thermus thermophilus HB8]

Score = 46.6 bits (109), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 34/109 (31%), Positives = 55/109 (50%), Gaps = 5/109 (4%)

Query 35 LTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKLQEQUELIKSSRATNDERVVLW 94
L+ + H+L LLA+ + +AE L++ P+ V+ L L+E+ L+K S D R V
Sbjct 36 LSPRKAHLLGLAKGVDLPSQLAEELLEVHPQSQVSHLLAEEEGLVKRSPDPQDRRKVKL 95

Query 95 SLTEKAVPVAKEHATHHEKT-LSTYQELGNKFTDEEQEVISKFLSALTE 142
LT P +E A E L+ + + + EQ + L LTE
Sbjct 96 FLT---PKGREAARTEALWLAVFGRRRLARLSPEEQAAFLRILRKLT 140

>ref|YP_293371.1| **G** regulatory protein, MarR [Ralstonia eutropha JMP134]
gb|AAZ65514.1| **G** regulatory protein, MarR [Ralstonia eutropha JMP134]
Length=150

GENE ID: 3607869 Reut_C6203 | regulatory protein, MarR
[Ralstonia eutropha JMP134]

Score = 46.6 bits (109), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 32/112 (28%), Positives = 58/112 (51%), Gaps = 1/112 (0%)

Query 6 QIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNA-KIAEKLKISP 64
+I Q +G + A N + + D+ +T Q IL+ L + ++T +++++ L I
Sbjct 15 RITQSVGFNLRARNTLLMEMDAALKDLDITGQQMGILLSLTQGVATTPFELSKVLGIDT 74

Query 65 AAVTKALKLQEQUELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLS 116
+T+ L KL+ + L+ SR+ +D RVV +LT+K VA+ K L+
Sbjct 75 GLMTRMLDKLETKGGLLSRSRSRSLDDRRVVNLTLQKGQEVARAPVVAAPKVLN 126

>ref|YP_001307422.1| **G** MarR family transcriptional regulator [Clostridium beijerinckii NCIMB 8052]
gb|ABR32466.1| **G** transcriptional regulator, MarR family [Clostridium beijerinckii NCIMB 8052]
Length=153

GENE ID: 5291510 Cbei_0278 | MarR family transcriptional regulator
[Clostridium beijerinckii NCIMB 8052]

Score = 46.6 bits (109), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 30/114 (26%), Positives = 62/114 (54%), Gaps = 1/114 (0%)

Query 32 DVKLITSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKLQEQUELIKSSRATNDER 90
D+ L ++ H++ + + NA I+++L ++ A++K KL ++ELIK + N++
Sbjct 40 DMGLMLSEIHVIDCIGKNQLINATFISKELNMTKGAIKSITSKLLKKELIKGNHLENNKK 99

Query 91 VVWLWSLTEKAVPVAKEHATHHEKTLSPTYQELGNKFTDEEQEVISKFLSALTEEF 144
+ ++LT + V K H H+ + ++ +K+ EE +I+ FL L E
Sbjct 100 EIYYTLAQGKEVFVKHEILHKIESEKFVKILSKYDKEELSIINSFLEDLISEL 153

>ref|ZP_02950515.1| transcriptional regulator, MarR family [Clostridium butyricum 5521]
gb|EDT74473.1| transcriptional regulator, MarR family [Clostridium butyricum 5521]
Length=145

Score = 46.2 bits (108), Expect = 8e-04, Method: Compositional matrix adjust.
Identities = 32/86 (37%), Positives = 48/86 (55%), Gaps = 2/86 (2%)

Query 17 FAENKHEILLGK-CESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKL 74
+A ++ I L K C LT TQ +L+L ++ ST +I ++L + +T LKK+
Sbjct 19 YAASREVIKLYKPCLDKFNLTQYVAMVLWEDEKSTVKEIGKRLHLDGSTLTPLLKKM 78

Annex 1

Query 75 QEQUELIKSSRATNDERVVLWSLTEKA 100
 + ELIK R ND+RVV+ L EK
 Sbjct 79 ESMELIKRYRDINDDRVIVELAEKG 104

>ref|NP_266269.1| **G** transcription regulator [Lactococcus lactis subsp. lactis II1403]
 gb|AAK04211.1|AE006249_8 **G** transcriptional regulator [Lactococcus lactis subsp. lactis II1403]
 Length=163

GENE ID: 1113719 rmaD | transcription regulator
 [Lactococcus lactis subsp. lactis II1403] (10 or fewer PubMed links)
 Score = 46.2 bits (108), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 26/98 (26%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

Query 41 HILMLAEQISTNAKIAEKLKISPAAVTKALKLQEQUELIKSSRATNDERVVLWSLTEKA 100
 HIL L ++ T ++A KL ++ VT+A++ L + + + + ++ +D++ + + LT K
 Sbjct 53 HILSALKEDLTGIELATKLSVTGGVTRAVQNLIKYQFLTTYQSESDKKKIFYHLTVKG 112

Query 101 VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS 138
 VA H H+ ++ +K+ ++E+ +I FLS
 Sbjct 113 RKVATIHDKMHKIMDIRLGQIFDKYNEQEKSIIILSFLS 150

>ref|YP_002352539.1| **G** transcriptional regulator, MarR family [Dictyoglomus turgidum DSM 6724]
 gb|ACK41925.1| **G** transcriptional regulator, MarR family [Dictyoglomus turgidum DSM 6724]
 Length=145

GENE ID: 7081680 Dtur_0640 | transcriptional regulator, MarR family
 [Dictyoglomus turgidum DSM 6724]

Score = 46.2 bits (108), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 33/118 (27%), Positives = 63/118 (53%), Gaps = 8/118 (6%)

Query 31 SDVKLTSTQEHIMLLAEQIS-TNAKIAEKLKISPAAVTKALKLQEQUELIKSSRATNDE 89
 S +KL Q IL+LL+E+ T +I E +KI P+ V ++++++ L+ + R D+
 Sbjct 26 SGLKLYRGQAPILLLSERDGLTQEIVENMKPSTVAIMIRRMKKRGLVITKRDEDK 85

Query 90 RVVWLWLSLTEKAVPVAKEHATHHEKTLSTYQE--LGNKFTDEEQEVISKFLSALTEEFQ 145
 R LT++ ++ +KT +E GN FT+EE+E + +L + + +
 Sbjct 86 RFSKVYLTDE---GRKFICKLKKTYKQLEEECFGN-FTEEERETLKNYLERIRDNL 138

>ref|ZP_01854255.1| probable marR-family transcription regulator [Planctomyces maris DSM 8797]
 gb|EDL59963.1| probable marR-family transcription regulator [Planctomyces maris DSM 8797]
 Length=159

Score = 46.2 bits (108), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 29/83 (34%), Positives = 46/83 (55%), Gaps = 2/83 (2%)

Query 26 LGKCESDVKLTSTQEHIMLLA--EQISTNAKIAEKLKISPAAVTKALKLQEQUELIKSS 83
 G+ + LT +Q ++L +L + + +IA ++ A+T L +LO QELIK +
 Sbjct 38 FGRLFREYGLTPSQYNVRILRGERKPMPMSLEIANRMIQVVPAITGLLDRLQAQELIKRN 97

Query 84 RATNDERVVLWLSLTEKAVPVAKE 106
 R T D RVV +T KA+ + KE
 Sbjct 98 RCTEDRRVVYIEITAKALKLKE 120

>ref|YP_773280.1| **G** MarR family transcriptional regulator [Burkholderia ambifaria AMMD]
 gb|ABI86946.1| **G** transcriptional regulator, MarR family [Burkholderia ambifaria AMMD]
 Length=164

GENE ID: 4309612 Bamb_1388 | MarR family transcriptional regulator
 [Burkholderia ambifaria AMMD]

Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/118 (26%), Positives = 59/118 (50%), Gaps = 4/118 (3%)

Query 28 KCESDVKLTSTQEHIMLLA-EQISTNAKIAEKLKISPAAVTKALKLQEQUELIKSSRAT 86
 + + ++ +T TQ +L ++A + ST A++A + I +AVT+ L +++++ L+ R+
 Sbjct 40 RTQEELGITGTQASMLFMIAVGRCSTAAELAREYGIDASAVTRLDRVEKRGLLSRVRSI 99

Query 87 NDERVVLWLSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
 D RVV LT++ +A+ L EL FT EE + L + +
 Sbjct 100 EDRRVVRLLELTDEGRALAERLPPVFRSVL---DELLGGFTPEEVGFLKSMRLRILSNY 154

>ref|ZP_01131766.1| transcriptional regulator, MarR family protein [Pseudoalteromonas tunicata D2]
 gb|EAR30132.1| transcriptional regulator, MarR family protein [Pseudoalteromonas tunicata D2]
 Length=163

Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 29/83 (34%), Positives = 47/83 (56%), Gaps = 1/83 (1%)

Query 28 KCESDVKLTSTQEHIMLLAEQISTNAK-IAEKLKISPAAVTKALKLQEQUELIKSSRAT 86

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Sbjct 24 K + LTS Q +L +++Q . K IAE++ +S A +T L +L+ +EL+ R+T
 KLSKETGLTSPQLLVQAISSQQDGVMVKEIAEQINLSSATITSILDRLIEIRELVIRERST 83
 Query 87 NDERVVLWLSLTEKAVPVAKEHAT 109
 D+R V SLT+K + K+ T
 Sbjct 84 TDKRRVGISLTDKGFDIICKDSPT 106

>ref|ZP_00238819.1| transcriptional regulator, MarR family [Bacillus cereus G9241]
 gb|EALI3614.1| transcriptional regulator, MarR family [Bacillus cereus G9241]
 Length=152

Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 27/85 (31%), Positives = 49/85 (57%), Gaps = 1/85 (1%)

Query 35 LTSTQEHIIMLLAEQISTNA-KIAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVL 93
 LT Q +IL +L ++ A K+A+K+ P+A+T +L +QEL++ +D RVV+
 Sbjct 35 LTPPQFYILKILDHYGASRATKLAKKMYVKPSAITVMIDRLIDQELVERYHDKDDRRVVI 94
 Query 94 WSLTEKAVPVAKEHATHHEKTLSTY 118
 LT+K +E T + ++ Y
 Sbjct 95 IELTKKGKARVEEAMTARNEHIAKY 119

>ref|YP_002467440.1| **G** transcriptional regulator, MarR family [Candidatus Methanospaerula palustris El-9c]
 gb|ACL17717.1| **G** transcriptional regulator, MarR family [Candidatus Methanospaerula palustris El-9c]
 Length=159

GENE ID: 7271351 Mpal_2438 | transcriptional regulator, MarR family
 [Candidatus Methanospaerula palustris El-9c]

Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 25/85 (29%), Positives = 47/85 (55%), Gaps = 0/85 (0%)

Query 56 IAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTL 115
 IA+ L ++P+A ++A+ KL + L+K R +ER V LT++ + H H++
 Sbjct 53 IADLLGVTPSAASQAVTKLAGRGLVKKVGRKRNEREVSELETDQGWVAYRYHEQTHKEIY 112
 Query 116 STYQELGNKFTDEEQEVISKFLSAL 140
 + E ++EE E+I++F +A
 Sbjct 113 TRTTERVGPLSEEELIARFFNAF 137

>ref|ZP_03547491.1| hypothetical protein BLAHAN_01259 [Blautia hansenii DSM 20583]
 gb|EED60137.1| hypothetical protein BLAHAN_01259 [Blautia hansenii DSM 20583]
 Length=168

Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 32/105 (30%), Positives = 53/105 (50%), Gaps = 4/105 (3%)

Query 41 HILMLLAEQISTN-AKIAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWSLTEK 99
 HI+ + E+ + N+ +A+ L++ +T A+ L++ + R+ D RVVL SLT K
 Sbjct 60 HIMEAIGEENAKNMSSVAKLSSVTVGTLTIAINGLVKKGYVARERSEEDRRVVVLISLTGK 119
 Query 100 AVPVAKEHAHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
 + H H+ + Q L DE+QE++ K L L E F
 Sbjct 120 GRKANEHHKKFHDMGI---QALLKDLDEQQEILVKSLNNLREFF 161

>ref|ZP_02891041.1| transcriptional regulator, MarR family [Burkholderia ambifaria IOP40-10]
 gb|EDT03378.1| transcriptional regulator, MarR family [Burkholderia ambifaria IOP40-10]
 Length=163

Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/118 (26%), Positives = 59/118 (50%), Gaps = 4/118 (3%)

Query 28 KCESDVKLTSTQEHIIMLLA-EQISTNAKIAEKLKISPAAVTKALKLQEQLIKSSRAT 86
 + + ++ +T TQ +L ++A + ST A++A + I +AVT+ L +++++ L+ R+
 Sbjct 40 RTQEEELGITGTQASMLFMIAVGKCASTAAELAREYGIDASAVTRLLDRVEKRGLLSRVRSI 99
 Query 87 NDERVVLWLSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
 D RVV LT++ +A+ L EL FT EE + L + +
 Sbjct 100 EDRRVVRLLELTDEGRELATERLPPVFRSVL---DELLGGFTPEEVGFLKSMLRRILSNY 154

>ref|YP_001808132.1| **G** MarR family transcriptional regulator [Burkholderia ambifaria MC40-6]
 gb|ACB63916.1| **G** transcriptional regulator, MarR family [Burkholderia ambifaria MC40-6]
 Length=164

GENE ID: 6177160 BamMC406_1428 | MarR family transcriptional regulator
 [Burkholderia ambifaria MC40-6]

Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/118 (26%), Positives = 59/118 (50%), Gaps = 4/118 (3%)

Query 28 KCESDVKLTSTQEHIIMLLA-EQISTNAKIAEKLKISPAAVTKALKLQEQLIKSSRAT 86
 + + ++ +T TQ +L ++A + ST A++A + I +AVT+ L +++++ L+ R+
 Sbjct 40 RTQEEELGITGTQASMLFMIAVGKCASTAAELAREYGIDASAVTRLLDRVEKRGLLSRVRSI 99

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Query 87 NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
 D RVV LT++ +A+ L EL FT EE + L + +
 Sbjct 100 EDRRVVRLTDEGRALAERLPPVFRSVL---DELLGGFTPEEVGFLKSMLRRILSNY 154

>ref|ZP_02906301.1| transcriptional regulator, MarR family [Burkholderia ambifaria MEX-5]
 gb|EDT42559.1| transcriptional regulator, MarR family [Burkholderia ambifaria MEX-5]
 Length=164

Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/118 (26%), Positives = 59/118 (50%), Gaps = 4/118 (3%)

Query 28 KCESDVKLTSQEHIMLLA-EQISTNAKIAEKLKISPAAVTKALKLQEQUELIKSSRAT 86
 + + ++ +T TO +L ++A + ST A++A + I +AVT+ L +++++ L+ R+
 Sbjct 40 RTQEELGITGTQASMLFMIAVGKCSTAAELAREYGIDASAVTRLLDRVEKGFLLSRVRSI 99

Query 87 NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
 D RVV LT++ +A+ L EL FT EE + L + +
 Sbjct 100 EDRRVVRLTDEGRALAERLPPVFRSVL---DELLGGFTPEEVGFLKSMLRRILSNY 154

>ref|ZP_02362996.1| transcriptional regulator, MarR family protein [Burkholderia oklahomensis C6786]
 Length=165

Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/126 (24%), Positives = 69/126 (54%), Gaps = 5/126 (3%)

Query 6 QIDQFLGTIMQFAEN-KHEILLGKCESDVKLTSQEHIMLLA-EQISTNAKIAEKLKIS 63
 QI+ +G +M + + + + +++++ +T TO +L +LA + ST A++A + I
 Sbjct 17 QINDSGVYLMMSRVKSLMTNMTQRTQTELGITGTQATMLFLAVGKCSTAAELAREYGID 76

Query 64 PAAVTALKLQEQUELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGN 123
 +A+T+ L +++++ L++ R++ D RVV LT++ + + L + + +
 Sbjct 77 ASAITRLLDRVEKGFLLQRVRSSEDRRVVRLTDEGRDLTRRMPAIFRSVL---DQVLD 133

Query 124 KFTDEE 129
 FT EE
 Sbjct 134 GFTPEE 139

>ref|NP_977055.1| **G** MarR family transcriptional regulator [Bacillus cereus ATCC 10987]
 gb|AAS39663.1| **G** transcriptional regulator, MarR family [Bacillus cereus ATCC 10987]
 Length=152

GENE ID: 2747926 BCE 0730 | MarR family transcriptional regulator
 [Bacillus cereus ATCC-10987] (10 or fewer PubMed links)

Score = 45.4 bits (106), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 27/85 (31%), Positives = 49/85 (57%), Gaps = 1/85 (1%)

Query 35 LTSTQEHIMLLAEQISTNA-KIAEKLKISPAAVTKALKLQEQUELIKSSRATNDERVVL 93
 LT Q +IL +L + + A K+A+K+ P+A+T + +L +QEL++ +D RVV+
 Sbjct 35 LTPPQFYILKILDHYGASRATKLAKKMYVKPSAITVMIDRIIDQELVERYHDKDDRRVVV 94

Query 94 WSLTEKAVPVAKEHATHHEKTLSTY 118
 LT+K +E T + ++ Y
 Sbjct 95 IELTKKGKARVEEAMTARNEHIAKY 119

>ref|NP_782475.1| **G** MarR family transcriptional regulator [Clostridium tetani E88]
 gb|AOO36412.1| **G** transcriptional regulator, marR family [Clostridium tetani E88]
 Length=154

GENE ID: 1058804 marR | MarR family transcriptional regulator
 [Clostridium tetani E88] (10 or fewer PubMed links)

Score = 45.4 bits (106), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 25/91 (27%), Positives = 50/91 (54%), Gaps = 0/91 (0%)

Query 51 STNAKIAEKLKISPAAVTKALKLQEQUELIKSSRATNDERVVLWSLTEKAVPVAKEHATH 110
 + +IA L I+ +AV+K +++++LQ++ LI SS+ +++++ + ++LT + + K+H
 Sbjct 50 ANGTQIANYLNITRSAVSKIIIRRLQKENLISSQKPDNKKEIFYTLTNEGNNIFKQHKQA 109

Query 111 HEKTLSTYQELGNKFTDEEQEVISKFLSALT 141
 HEK + + E+E + KFL
 Sbjct 110 HEKWEIFRDTKFLKTISTNEKETVFKFLKKFN 140

>ref|ZP_03570809.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD2M]

>ref|ZP_03577696.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD2]

>ref|ZP_03586132.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD1]

>gb|EED99839.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD1]

>gb|EEE07966.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD2]

>gb|EEE14096.1| transcriptional regulator, MarR family [Burkholderia multivorans CGD2M]

Length=164

Annex 1

Score = 45.1 bits (105), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 32/118 (27%), Positives = 60/118 (50%), Gaps = 4/118 (3%)

Query 28 KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKLQEQUELIKSSRAT 86
 + + ++ +T TQ +L ++A + ST A++A + I +AVT+ L +++++ L+ R+
 Sbjct 40 RTQEELGITGTQASMLFMIAVGKCSTAAELAREYAIADASAVTRLDRVEKRGLLCRVRSV 99
 D RVV LT++ +A+ L Q LG FT EE + L + +
 Query 87 NDERVVLWSLTEKAVPVAKEHATHHEKTTLSTYQELGNKFTDEEQEVISKFLSALTEEF 144
 Sbjct 100 EDRRVVRLTELTDGRALAERLPAIFRSVLD--QLGG-FTPEEVGFLKSMLRRILSNY 154

>ref|YP_001119315.1| **G** MarR family transcriptional regulator [Burkholderia vietnamiensis G4]
 gb|ABO54480.1| **G** transcriptional regulator, MarR family [Burkholderia vietnamiensis G4]
 Length=163

GENE ID: 4953186 Bcep1808_1472 | MarR family transcriptional regulator
 [Burkholderia vietnamiensis G4]

Score = 45.1 bits (105), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 35/126 (27%), Positives = 66/126 (52%), Gaps = 5/126 (3%)

Query 6 QIDQFLGTIMQFAENKHEILLG-KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKIS 63
 QI+ +G +M + + L+ + + ++ +T TQ +L ++A + ST A++A + I
 Sbjct 17 QINDSVGYLMSRVRKSVMTNLVQTQEEELGITGTQASMLFMIAVGKCSTAAELAREYRID 76
 PAAVTALKLQEQUELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTTLSTYQELGN 123
 +AVT+ L +++++ L+ R+ D RVV LT++ +A+ L EL
 Sbjct 77 ASAVENTLDRVEKRGLLSRVRSIEDRRVVRLTELTDGRALAERLPPVFRSVL---DELLE 133
 Query 124 KFTDEE 129
 FT EE
 Sbjct 134 GFTPEE 139

>ref|YP_002418276.1| **G** Histone acetyltransferase HPA2 and related acetyltransferases [Vibrio splendidus LGP32]
 emb|CAV19992.1| **G** Histone acetyltransferase HPA2 and related acetyltransferases [Vibrio splendidus LGP32]
 Length=301

GENE ID: 7162224 vs 2735 | Histone acetyltransferase HPA2 and related acetyltransferases [Vibrio splendidus LGP32]

Score = 45.1 bits (105), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 35/117 (29%), Positives = 60/117 (51%), Gaps = 1/117 (0%)

Query 25 LLGKCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKLQEQUELIKSSR 84
 +L K +D L Q H L+ L +Q T +A+KL I + ++A+ L+ LI++S
 Sbjct 19 MLDKDCGDIALPPIQAHTLIELEQQPLTVNQLADKLNIDKSNASRAVNNLAKNSLIQTSP 78
 ATNDERVVLWSLTEKA-VPVAKEHATHHEKTTLSTYQELGNKFTDEEQEVISKFLSAL 140
 ND+R V+ S+T++ +AK H ++ S + L T + I +L AL
 Sbjct 79 HPNDKRVSVASVTDQGKNTLAKLHNQNQFYDSVLEHLTEAQVQVSGGIEHYLKAL 135

>ref|ZP_02355848.1| transcriptional regulator, MarR family protein [Burkholderia oklahomensis EO147]
 Length=165

Score = 45.1 bits (105), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 31/126 (24%), Positives = 69/126 (54%), Gaps = 5/126 (3%)

Query 6 QIDQFLGTIMQFAEN-KHEILLGKCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKIS 63
 QI+ +G +M + + + + +++++ +T TQ +L +LA + ST A++A + I
 Sbjct 17 QINDSVGYLMSRVRKSLSMTNMTQRTQTELGITGTQATMLFMIAVGKCSTAAELAREYRID 76
 PAAVTALKLQEQUELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTTLSTYQELGN 123
 +A+T+ L +++++ L++ R++ D RVV LT++ + + L ++ +
 Sbjct 77 ASAVENTLDRVEKRGLLQRVRSSEDRRVVRLTELTDGRALRMPAIFRSVLD---DQVLD 133
 Query 124 KFTDEE 129
 FT EE
 Sbjct 134 GFTPEE 139

>ref|YP_443075.1| **G** MarR family transcriptional regulator [Burkholderia thailandensis E264]
 ref|ZP_02374954.1| transcriptional regulator, MarR family protein [Burkholderia thailandensis TXDOH]
 ref|ZP_02388872.1| transcriptional regulator, MarR family protein [Burkholderia thailandensis Bt4]
 gb|ABC39239.1| **G** transcriptional regulator, MarR family [Burkholderia thailandensis E264]
 Length=165

GENE ID: 3849294 BTH_I2558 | MarR family transcriptional regulator
 [Burkholderia thailandensis E264] (10 or fewer PubMed links)

Score = 44.7 bits (104), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 33/126 (26%), Positives = 67/126 (53%), Gaps = 5/126 (3%)

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Query 6 QIDQFLGTIMQFAEN-KHEILLGKCESDVQLTSTQEHIMLLA-EQISTNAKIAEKLKIS 63
 Sbjct 17 QINDSGYLMRSRVKSLMTNVTQRTQTELGITGTQATMLFMLAVGKCSTAAELAREYGD 76

Query 64 PAAVTKALKKLQEQUELIKSSRATNDERVVLSLTEKAVPVAKEHATHHEKTLSTYQELGN 123
 Sbjct 77 ASAITRLLDRVEKRGLLQRVRSSEDRRVVRLELTDEGRELTKRMPEIFRSVLDQVLE--- 133

Query 124 KFTDEE 129
 Sbjct 134 GFTPSEE 139

>ref|ZP_02633998.1| transcriptional regulator, MarR family [Clostridium perfringens E str. JGS1987]
 ref|ZP_02636384.1| transcriptional regulator, MarR family [Clostridium perfringens B str. ATCC 3626]
 ref|ZP_02643088.1| transcriptional regulator, MarR family [Clostridium perfringens NCTC 8239]
 7 more sequence titles

ref|ZP_02629009.2| transcriptional regulator, MarR family [Clostridium perfringens C str. JGS1495]
 ref|ZP_02954000.1| transcriptional regulator, MarR family [Clostridium perfringens D str. JGS1721]
 gb|EDS81585.1| transcriptional regulator, MarR family [Clostridium perfringens C str. JGS1495]
 gb|EDT13394.1| transcriptional regulator, MarR family [Clostridium perfringens E str. JGS1987]
 gb|EDT23419.1| transcriptional regulator, MarR family [Clostridium perfringens B str. ATCC 3626]
 gb|EDT71039.1| transcriptional regulator, MarR family [Clostridium perfringens D str. JGS1721]
 gb|EDT77904.1| transcriptional regulator, MarR family [Clostridium perfringens NCTC 8239]
 Length=154

Score = 44.7 bits (104), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 33/99 (33%), Positives = 50/99 (50%), Gaps = 5/99 (5%)

Query 48 EQISTNAKIAEKLKISPAAVTKALKLQEQUELIKSSRATNDERVVLSLTEKAVPVAKEH 107
 Sbjct 49 EKARTMSEVALDLKITVGTLTTAINKLIKGYVNRRRIEEDRRVVMIELTEKGTLAYKVH 108

Query 108 ATHHEKTLS-TYQELGNKFTDEEQEVISKFLSALTEEFQ 145
 Sbjct 109 EKFHEEMIDHVLEELGVSS---EEEVLISSLKDLDKFFQ 143

>ref|YP_001374721.1| **G** MarR family transcriptional regulator [Bacillus cereus subsp. cytotoxins NVH 391-98]
 gb|ABS21726.1| **G** transcriptional regulator, MarR family [Bacillus cereus subsp. cytotoxins NVH 391-98]
 Length=136

GENE ID: 5344927 Bcer98_1405 | MarR family transcriptional regulator
 [Bacillus cereus subsp. Cytotoxins NVH 391-98]

Score = 44.7 bits (104), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 37/119 (31%), Positives = 62/119 (52%), Gaps = 4/119 (3%)

Query 28 KCESDVVLTSTQEHIMLLAEQISTN-AKIAEKLKISPAAVTKALKLQEQUELIKSSRAT 86
 Sbjct 16 RCEYENNLSHQAIRILQITSREAETTISKIASELNLSHNTASEHVVKRLIQKDLILKERNK 75

Query 87 NDERVVLSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ 145
 Sbjct 76 KDERVVNLALTAKGEALIKHTLLDEKKLKI---LESQLSKEEQQIIEQAFSILAKEAQ 131

>ref|YP_819461.1| **G** transcriptional regulator [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]
 gb|ABJ63088.1| **G** Transcriptional regulator [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]
 Length=146

GENE ID: 4423731 LEUM_2018 | transcriptional regulator
 [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]
 (10 or fewer PubMed links)

Score = 44.7 bits (104), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 30/84 (35%), Positives = 46/84 (54%), Gaps = 5/84 (5%)

Query 34 KLTSTOEHIMLL-AEQISTNAKIAEKLKISPAAVTKALKLQEQUELIKSSRATNDERRV 92
 Sbjct 32 KINSTQAHLLMLLKILQSQTNTELAAAMNLSPAITKAIKNLMRHYHYIAVVDDSDKRST 91

Query 93 LWSLTEKAVPVVA---KEHATHHE 112
 Sbjct 92 HYLLTEDGEKLAQLHEQAHAMTHD 115

>ref|ZP_02027443.1| hypothetical protein EUBVEN_02713 [Eubacterium ventriosum ATCC 27560]

gb|EDM50067.1| hypothetical protein EUBVEN_02713 [Eubacterium ventriosum ATCC 27560]
Length=151

Score = 44.7 bits (104), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 27/90 (30%), Positives = 53/90 (58%), Gaps = 3/90 (3%)

Query 56 IAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTL 115
IA+K+KI+ ++T ++ L ++ ++ +R+ D R+V +LTEK + K H HEK
Sbjct 60 IAKKMKITVGSLTTSMNSLVKKHYVERNRSEEDRRIVNITLTEKGKAYKHHEEFHEK-- 117

Query 116 STYQELGNKFTDEEQEVISKFLSALTEEFQ 145
O ++ +++E +V+ K L+ L++ F
Sbjct 118 -MSQAAISEMSEDEVKVLLKSLNNLSKFFH 146

Select All [Get selected sequences](#) [Distance tree of results](#)



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By facsimile
+ confirmation by e-mail

THE NATH LAW GROUP
112 South West Street
US-ALEXANDRIA, VA 22314
ETATS-UNIS D'AMERIQUE

Attention : M. William E. BEAUMONT

Paris, March 5, 2009

UNITED STATES OF AMERICA - PATENT APPLICATION No. 10/525,449
filed on : August 29, 2003

In the name of: INSTITUT NATIONAL DE LA RECHERCHE
AGRONOMIQUE.

For : « Zinc-regulated prokaryotic expression cassettes. »

Invention : POQUET Isabelle, LLULL Daniel

Y/Ref.: 1169-034

O/Ref.: MJP/DG/md - F053900116/US/PCT

Dear Sir,

We refer to your letter of October 31, 2008 transmitting us the 1st Office Action
issued in relation with the above-referred application.

We have discussed this case with the applicant, and beg you to find herein enclosed
our comments and instructions concerning this application.

Since we believe that an interview with the Examiner will be necessary in order to
discuss the objections and the possible amendments to the claims, you may request a
third month extension of time.

Please acknowledge receipt of this letter by return.

In the meantime, we are,

Very truly yours,

M.J. VIALLE-PRESLES

B. ORES

Encl. : - Memorandum, and
- Annexes (only by e-mail).

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380 823 79 R.C.S. Paris

U.S Application 10/1525449

MEMORANDUM OF INSTRUCTIONS FOR RESPONDING THE OFFICE ACTION OF OCTOBER 7, 2008

1) Claims objections:

We beg you to amend the claims as requested by the Examiner. Concerning claim 15, it differs from claim 12 in that the expression cassette does not comprise the sequence encoding the ZitR repressor (cf § [0025] to [0027] of the instant application), and can be used to obtain constitutive expression of a protein of interest in bacterial strains wherein the endogenous ZitR repressor is inactivated (cf. § [0053] of the instant application)

2) Rejection under 35 USC § 112.

We wish to point out that the definition "at least 80% identity with the *Lactococcus lactis* ZitR protein GENBANK AAK06214" does not encompass a broad variety of proteins.

The results of BLAST searches using GENBANK AAK06214 as a query are enclosed therein. A first search was performed against all the protein sequences available in the nr database (all known protein sequences, including the complete sequences of various bacteria). The enclosed results (Annex 1) show that the only proteins having more than 80% identity with GENBANK AAK06214 (which is the ZitR protein of *Lactococcus lactis* subsp. *lactis* II1403), are the ZitR proteins of *Lactococcus lactis* subsp. *cremoris* SK11 (89% identity) and the ZitR proteins of *Lactococcus lactis* subsp. *cremoris* MG1363 (88% identity).

A second search was performed against the whole genome sequences of *Lactococcus lactis* subsp. *lactis* II1403, *Lactococcus lactis* subsp. *cremoris* SK11 and *Lactococcus lactis* subsp. *cremoris* MG1363. The enclosed results (Annex 2) show that the only lactococcal proteins having more than 80% identity with GENBANK AAK06214, are the ZitR proteins of *Lactococcus lactis* subsp. *cremoris* SK11 (89% identity) and the ZitR proteins of *Lactococcus lactis* subsp. *cremoris* MG1363 (88% identity).

Therefore, obtaining a nucleotide sequence encoding a protein having more than 80% identity with GENBANK AAK06214 would not have required require undue experimentation for one of skill in the art. He would have easily obtained it by routine screening of a lactococcal DNA library with a probe derived from the nucleotide sequence encoding GENBANK AAK06214 (or from nucleotides 357-794 of SEQ ID NO:2), and would inevitably have found the orthologs of GENBANK AAK06214.

We beg you to request an interview with the Examiner in order to discuss this issue of enablement. If necessary, you may amend paragraph b) of claim 12 so as to

specify that the polypeptide is a lactococcal polypeptide, and/or to indicate a higher percent of identity (85% rather than 80%) with GENBANK AAK06214.

3) Rejection under 35 USC § 102.

We beg you to insert in claims 12 and 15 the same disclaimer as in claim 18, which excludes the cassette and vector of POQUET et al.

BLAST Basic Local Alignment Search Tool

[Formatting options](#) [Download](#)

gb|AAK06214| (145 letters)

Results for: | gb|AAK06214.1 zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis II1403](145aa)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|12725171|gb|AAK06214.1|AE006439_11

Description

zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis II1403]

Molecule type

amino acid

Query Length

145

Database Name

3 databases

Description

Program

BLASTP 2.2.19+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#)

Search Parameters

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats2	
Low Complexity Filter	Yes
Filter string	L;
Genetic Code	1
Window Size	40

Database

Posted date	Mar 2, 2009 5:57 PM
Number of letters	2,055,736
Number of sequences	7,259
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.310848	0.267
K	0.124161	0.041

H 0.32399 0.14

Results Statistics

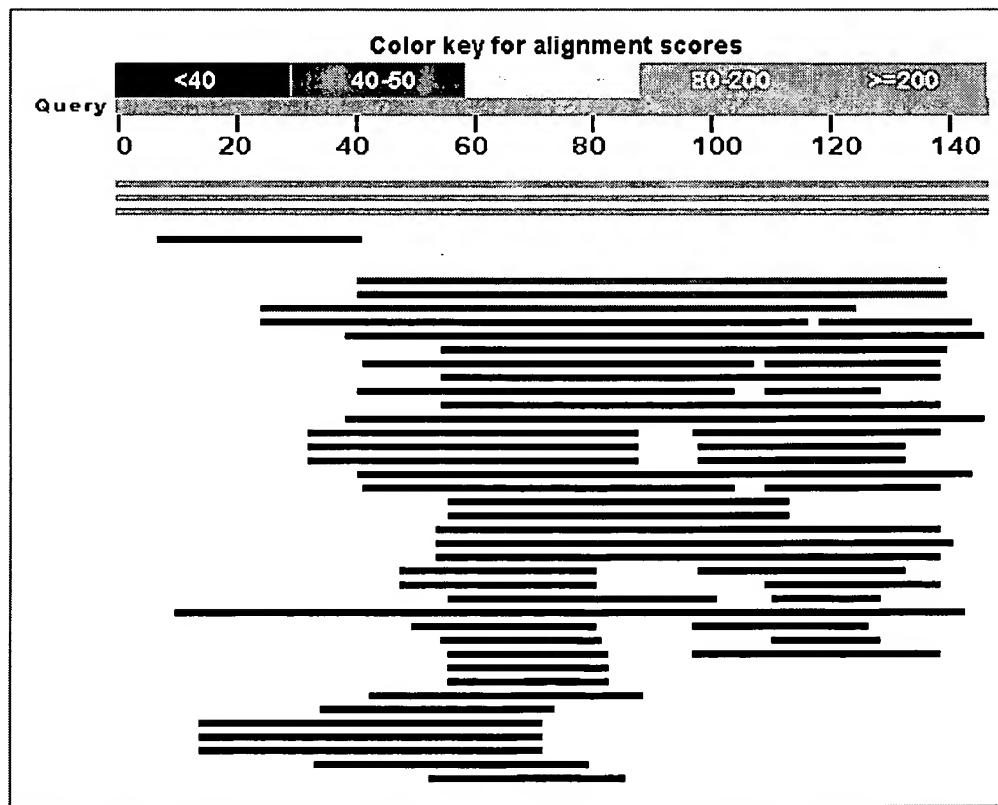
Length adjustment 78 .
 Effective length of query 67
 Effective length of database 1489534
 Effective search space 99798778
 Effective search space used 99798778

Graphic Summary

Distribution of 58 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Annex 2

Descriptions

		Score (Bits)	E Value	
	Sequences producing significant alignments:			
ref NP_266273.1	zinc transport transcription regulator [Lactococcus lactis subsp. ...]	29.1	2e-80	G
ref YP_811979.1	transcriptional regulator [Lactococcus lactis subsp. ...]	16.8	2e-73	G
ref YP_001032643.1	transcriptional regulator of the zit operon [Lactococcus lactis subsp. ...]	16.7	3e-73	G
ref YP_001032131.1	MarR family transcriptional regulator [Lactococcus lactis subsp. ...]	53.9	6e-09	G
ref YP_808725.1	transcriptional regulator [Lactococcus lactis subsp. ...]	51.2	4e-08	G
ref NP_266264.1	transcription regulator [Lactococcus lactis subsp. ...]	51.2	4e-08	G
ref YP_808147.1	transcriptional regulator [Lactococcus lactis subsp. ...]	50.4	7e-08	G
ref YP_001031452.1	MarR family transcriptional regulator [Lactococcus lactis subsp. ...]	49.3	1e-07	G
ref NP_266269.1	transcription regulator [Lactococcus lactis subsp. ...]	46.2	1e-06	G
ref NP_267626.1	transcription regulator [Lactococcus lactis subsp. ...]	41.2	4e-05	G
ref YP_001032345.1	MarR family transcriptional regulator [Lactococcus lactis subsp. ...]	38.9	2e-04	G
ref YP_808179.1	transcriptional regulator [Lactococcus lactis subsp. ...]	37.0	9e-04	G
ref NP_266463.1	MarR family transcriptional regulator [Lactococcus lactis subsp. ...]	36.2	0.001	G
ref NP_266747.1	transcription regulator [Lactococcus lactis subsp. ...]	35.8	0.002	G
ref YP_001031675.1	MarR family transcriptional regulator [Lactococcus lactis subsp. ...]	35.4	0.002	G
ref NP_266396.1	MarR family transcriptional regulator [Lactococcus lactis subsp. ...]	35.4	0.002	G
ref YP_808372.1	MarR family transcriptional regulator [Lactococcus lactis subsp. ...]	35.4	0.002	G
ref YP_001031774.1	transcriptional regulator [Lactococcus lactis subsp. ...]	35.0	0.003	G
ref YP_001031679.1	putative transcriptional regulator [Lactococcus lactis subsp. ...]	32.3	0.017	G
ref YP_808573.1	BadM/Rrf2 family transcriptional regulator [Lactococcus lactis subsp. ...]	32.3	0.018	G
ref NP_245714.1	hypothetical protein L153086 [Lactococcus lactis subsp. ...]	32.3	0.018	G
ref YP_001033090.1	MarR family transcriptional regulator [Lactococcus lactis subsp. ...]	31.6	0.031	G
ref YP_808765.1	MarR family transcriptional regulator [Lactococcus lactis subsp. ...]	31.6	0.034	G
ref YP_808795.1	MarR family transcriptional regulator [Lactococcus lactis subsp. ...]	31.2	0.044	G
ref NP_266926.1	MarR family transcriptional regulator [Lactococcus lactis subsp. ...]	31.2	0.045	G
ref YP_001032909.1	MarR family transcriptional regulator [Lactococcus lactis subsp. ...]	28.9	0.18	G
ref YP_001032520.1	MarR family transcriptional regulator [Lactococcus lactis subsp. ...]	28.1	0.31	G
ref NP_267064.1	transcription regulator [Lactococcus lactis subsp. ...]	28.1	0.35	G
ref YP_001032533.1	transcriptional regulator [Lactococcus lactis subsp. ...]	22.1	0.38	G
ref YP_808312.1	Mn-dependent transcriptional regulator [Lactococcus lactis subsp. ...]	22.1	0.38	G
ref NP_267461.1	transcription regulator [Lactococcus lactis subsp. ...]	22.7	0.42	G
ref NP_267496.1	transcription regulator [Lactococcus lactis subsp. ...]	22.3	0.61	G
ref NP_266753.1	NADPH-flavin oxidoreductase [Lactococcus lactis subsp. ...]	22.3	0.67	G
ref NP_267412.1	metalloregulator [Lactococcus lactis subsp. ...]	22.6	1.1	G
ref YP_001031697.1	putative cobalt ABC transporter ATP-binder [Lactococcus lactis subsp. ...]	22.2	1.2	G
ref NP_266873.1	quinone oxidoreductase [Lactococcus lactis subsp. ...]	25.4	2.4	G
ref NP_268402.1	alkylphosphonate uptake protein [Lactococcus lactis subsp. ...]	25.4	2.4	G
ref YP_808109.1	transcriptional repressor CodY [Lactococcus lactis subsp. ...]	24.6	3.4	G
ref YP_001031533.1	transcriptional repressor CodY [Lactococcus lactis subsp. ...]	24.6	3.4	G
ref NP_266317.1	transcriptional repressor CodY [Lactococcus lactis subsp. ...]	24.6	3.5	G
ref NP_266838.1	intercellular adhesion protein [Lactococcus lactis subsp. ...]	24.6	3.6	G
ref NP_266710.1	transcription regulator [Lactococcus lactis subsp. ...]	24.6	3.6	G
ref NP_266438.1	amino acid amidohydrolase [Lactococcus lactis subsp. ...]	24.6	4.1	G
ref YP_808446.1	lysyl-tRNA synthetase [Lactococcus lactis subsp. ...]	24.6	4.3	G
ref YP_001031741.1	lysyl-tRNA synthetase [Lactococcus lactis subsp. ...]	24.3	4.7	G
ref NP_266529.1	lysyl-tRNA synthetase [Lactococcus lactis subsp. ...]	24.3	4.7	G
ref YP_001031907.1	NADPH-flavin oxidoreductase [Lactococcus lactis subsp. ...]	24.3	5.2	G
ref YP_808603.1	NADPH-flavin oxidoreductase [Lactococcus lactis subsp. ...]	24.3	5.5	G
ref NP_266829.1	exported serine protease [Lactococcus lactis subsp. ...]	23.9	6.1	G
ref YP_001033660.1	housekeeping protease [Lactococcus lactis subsp. ...]	23.9	6.5	G
ref YP_811995.1	trypsin-like serine protease [Lactococcus lactis subsp. ...]	23.9	6.6	G
ref NP_268332.1	hypothetical protein L35545 [Lactococcus lactis subsp. ...]	23.5	7.5	G

		Annex 2
ref NP_266337.1	hypothetical protein L39650 [Lactococcus lac...]	23.5
ref YP_001032772.1	superfamily II DNA/RNA helicase [Lactococ...]	23.5
ref YP_001033122.1	quinone oxidoreductase [Lactococcus lacti...]	23.5
ref YP_008733.1	quinone oxidoreductase [Lactococcus lactis s...]	23.5
ref YP_796521.1	hypothetical protein LACR_C57 [Lactococcus l...]	23.5
ref YP_811979.1	hypothetical protein LACR_2554 [Lactococcus ...]	23.1
		10.0

Alignments Select All Get selected sequences Distance tree of results

>ref|NP_268273.1| **G** zinc transport transcription regulator [Lactococcus lactis subsp. lactis I11403]
Length=145

GENE ID: 1115793 zitR | zinc transport transcription regulator [Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 291 bits (744), Expect = 2e-80, Method: Compositional matrix adjust.
Identities = 145/145 (100%), Positives = 145/145 (100%), Gaps = 0/145 (0%)

Query 1	MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLSTQEHI MLLAEQISTNAKIAEKL	60
Sbjct 1	MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLSTQEHI MLLAEQISTNAKIAEKL	60
Query 61	KISPAAVTKALKKLQEQLIKSSRATNDERVVLWSLTEKA VPVAKEHATHHEKTLSTYQE	120
Sbjct 61	KISPAAVTKALKKLQEQLIKSSRATNDERVVLWSLTEKA VPVAKEHATHHEKTLSTYQE	120
Query 121	LGNKFTDEEQEVISKFLSALTEEFQ 145	
Sbjct 121	LGNKFTDEEQEVISKFLSALTEEFQ 145	

>ref|YP_811979.1| **G** transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=145

GENE ID: 4433026 LACR_2420 | transcriptional regulator [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 268 bits (685), Expect = 2e-73, Method: Compositional matrix adjust.
Identities = 130/145 (89%), Positives = 141/145 (97%), Gaps = 0/145 (0%)

Query 1	MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLSTQEHI MLLAEQISTNAKIAEKL	60
Sbjct 1	MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLSTQEHI LM+LA ++STNA+IAE+L	60
Query 61	KISPAAVTKALKKLQEQLIKSSRATNDERVVLWSLTEKA VPVAKEHATHHEKTLSTYQE	120
Sbjct 61	KISPAAVTKALKKLQEQLIKSSRATNDERVVLWSLTEKA VPVAKEHA HHEKTLSTYQE	120
Query 121	LGNKFTDEEQEVISKFLSALTEEFQ 145	
Sbjct 121	LGDKFTDEEQKVISQFLSVLTEEFR 145	

>ref|YP_001033643.1| **G** transcriptional regulator of the zit operon [Lactococcus lactis subsp. cremoris MG1363]
Length=145

GENE ID: 4799067 zitR | transcriptional regulator of the zit operon [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 267 bits (682), Expect = 3e-73, Method: Compositional matrix adjust.
Identities = 129/145 (88%), Positives = 141/145 (97%), Gaps = 0/145 (0%)

Query 1	MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLSTQEHI MLLAEQISTNAKIAEKL	60
Sbjct 1	MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLSTQEHI LM+LA ++STNA+IAE+L	60
Query 61	KISPAAVTKALKKLQEQLIKSSRATNDERVVLWSLTEKA VPVAKEHATHHEKTLSTYQE	120
Sbjct 61	KISPAAVTKALKKLQEQLIKSSRATNDERVVLWSLTEKA IPVAKEHAAHHEKTLSTYQE	120
Query 121	LGNKFTDEEQEVISKFLSALTEEFQ 145	
Sbjct 121	LGDKFTDEEQKVISQFLSVLTEEFR 145	

>ref|YP_001033131.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=295

GENE ID: 4797387 rmaB | MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 53.9 bits (128), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 38/101 (37%), Positives = 54/101 (53%), Gaps = 3/101 (2%)

Query 42	ILMLLAEQISTNAKIAEKLKISPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKAV	101
	++ L E TNA+IAE L I P++VT +K+L+E E++ + ND+RV LTEK	
Sbjct 47	LVELWNEDGLTNAEIAELLDIKPSSVTTQVKQLEEAEMVIRKQDENDKRVNRIFLTEKGR	106
Query 102	PVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTE	142
	+ T H T GN TDEEQE ++ + L E	
Sbjct 107	EAQETRDTMHNDISETI--FGN-LTDEEQEQLANLMEKLVE	144

>ref|YP_808725.1| **G** transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=292

GENE ID: 4432217 LACR_0742 | transcriptional regulator [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 51.2 bits (121), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 35/91 (38%), Positives = 50/91 (54%), Gaps = 3/91 (3%)

Query 52	TNAKIAEKLKISPAAVTKALKLQEELIKSSRATNDERVVLWSLITEKAVPVAKEHATHH	111
	TNA+IAE L I P++VT +K+L+E E++ + ND+RV LTEK + T H	
Sbjct 57	TNAEIAELLDIKPSSVTAQVKQLEEAEMVIRKQDENDKRVNRIFLTEKGREAQETRDTMH	116
Query 112	EKTLS TYQELGNKFTDEEQEVISKFLSALTE	142
	T GN TDEEQE ++ + L E	
Sbjct 117	NDISETI--FGN-LTDEEQKQLANLMEKLVE	144

>ref|NP_266864.1| **G** transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=291

GENE ID: 1114333 rmaB | transcription regulator [Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 51.2 bits (121), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 35/91 (38%), Positives = 50/91 (54%), Gaps = 3/91 (3%)

Query 52	TNAKIAEKLKISPAAVTKALKLQEELIKSSRATNDERVVLWSLITEKAVPVAKEHATHH	111
	TNA+IAE L I P++VT +K+L+E E++ + ND+RV LT+K + T H	
Sbjct 57	TNAEIAELLDIKPSSVTAQVKQLEEAEMVIRKQDENDKRVNSRIFLTDKGREAQETRDTMH	116
Query 112	EKTLS TYQELGNKFTDEEQEVISKFLSALTE	142
	T GN TDEEQE ++ + L E	
Sbjct 117	NDISETI--FGN-LTDEEQKQLANLMEKLVE	144

>ref|YP_808147.1| **G** transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=169

GENE ID: 4432499 LACR_0099 | transcriptional regulator [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 50.4 bits (119), Expect = 7e-08, Method: Compositional matrix adjust.
Identities = 27/98 (27%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

Query 41	HILMLLAEQISTNAKIAEKLKISPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKA	100
	HIL L ++ T ++A KL ++ VT+A++ L + + + + + A ND++ + + + T K	
Sbjct 53	HILSALTKKDLTGIELATKLSVTRGGVTRAVQNLIKHQFLTTYQADNDKKKIYYHITTKG	112
Query 101	VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS	138
	+ VA H H+ ++ +K+ + E+ +I FLS	
Sbjct 113	LKVASIHDKMHKIMDLKLGQIFDKYNENEKSIIILNFLS	150

>ref|YP_001031482.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=172

GENE ID: 4798609 rmaD | MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 49.3 bits (116), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 26/98 (26%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

Query 41	HILMLLAEQISTNAKIAEKLKISPAAVTKALKLQEELIKSSRATNDERVVLWSLTEKA	100
	HIL L ++ T ++A KL ++ VT+A++ L + + + + + A ND++ + + + T K	
Sbjct 56	HILSALTKKDLTGIELATKLSVTRGGVTRAVQNLIKHQFLTTYQADNDKKKIYYHITTKG	115
Query 101	VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS	138
	+ VA H H+ ++ +K+ + E+ +I FLS	
Sbjct 116	LKVASIHDKMHKIMDLKLGQIFDKYNENDKSIIILNFLS	153

>ref|NP_266269.1| **G** transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=163

GENE ID: 1113719 rmaD | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 46.2 bits (108), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 26/98 (26%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

Query 41	HILMLLAEQISTNAKIAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWSLTEKA	100
	HIL L ++ T ++A KL ++ VT+A++ L + + + + + + +D++ + + LT K	
Sbjct 53	HILSALTKEDELTGIELATKLSVTRGGVTRAVQNLKYQFLTTYQSESDDKKKIFYHLTVKKG	112
Query 101	VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS	138
	VA H H+ + + +K+ ++E+ +I FLS	
Sbjct 113	RKVATIHDKMHKIMDIRLGQIFDKYNEQEKSIIILSFLS	150

>ref|NP_267628.1| **G** transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=356

GENE ID: 1115129 rmaC | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 41.2 bits (95), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 29/100 (29%), Positives = 52/100 (52%), Gaps = 1/100 (1%)

Query 25	LLGKCESDVKLTSTQEHIMLL-AEQISTNAKIAEKLKISPAAVTKALKLQEQLIKSS	83
	+ K E + T+ ++M+L + + + + +LKI AAVT+ LK L+E+ L+K	
Sbjct 20	MTAKFEKSTGYSITRYQLMMILKCKGRCSQSQLQNELKIDSAAVTRHLKLLEEKNLVKRE	79
Query 84	RATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGN	123
	R + R V +T+KA A H+ +L Q++ N	
Sbjct 80	RNKENNREVFVEITDKAKNDLALCAKKHDDSLDESQQILN	119

>ref|YP_001032345.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=139

GENE ID: 4798214 rmaC | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 38.9 bits (89), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 25/92 (27%), Positives = 49/92 (53%), Gaps = 1/92 (1%)

Query 25	LLGKCESDVKLTSTQEHIMLL-AEQISTNAKIAEKLKISPAAVTKALKLQEQLIKSS	83
	+ K E + T+ ++M+L + + + + +LKI AAVT+ LK L+E+ L+K	
Sbjct 20	MTAKFEKSTGFSITRYQLMMILKCKGRCSQTQLQNELKIDSAAVTRHLKLLEEKNLVKRQ	79
Query 84	RATNDERVVLWSLTEKAVPVAKEHATHHEKTL	115
	R ++ R V +T++A + A H+ ++	
Sbjct 80	RNKDNNREVFVEITDEAKADLERCAREHDNSV	111

>ref|YP_808479.1| **G** transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=166

GENE ID: 4433047 LACR_0453 | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 37.0 bits (84), Expect = 9e-04, Method: Compositional matrix adjust.
Identities = 31/111 (27%), Positives = 54/111 (48%), Gaps = 13/111 (11%)

Query 39	QEHIMLLAEQISTNAKIAEK----LKISPAAVTKALKLQEQLIKSSRATNDERVVL	93
	Q IL +L E N+K+ +K L + P + ++ +KKL+ + + I + D+R +	
Sbjct 43	QGQILNILME---NSKMTQKNLVAQLDMRPQSASEMIKKLEKKQFISRKDAQDKRGFI	98
Query 94	WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF	144
	SLTEK V +E A E + FT+EE+ ++ + L E	
Sbjct 99	ISLTEKGKAVLEESAQTELVPG---IMTSFTEEEKIEFARLIGKLQSEL	145

>ref|NP_266463.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
Length=159

GENE ID: 1113917 napB | MarR family transcriptional regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 36.2 bits (82), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 23/84 (27%), Positives = 46/84 (54%), Gaps = 0/84 (0%)

Query 55	KIAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKT	114
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Annex 2

Sbjct 60 K+A L ++ A +K KKL ++ L++S + + + + + LT++ + H + H+K
 Sbjct 60 KLAHHLYMTRGAASKIAKKLLKKNLVESYQIPQNKKEIYFRLTKEGQEINDRHESLHQKF 119

Query 115 LSTYQELGNKFTDEEQEVISKFLS 138
 Sbjct 120 SEKDQVIFDELTDSEVSNILKFLN 143

>ref|NP_266747.1| **G** transcription regulator [Lactococcus lactis subsp. lactis I11403]
 Length=143

GENE ID: 1114211 rmaJ | transcription regulator
 [Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 35.8 bits (81), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 23/65 (35%), Positives = 33/65 (50%), Gaps = 0/65 (0%)

Query 42 IMLLAAEQISTNAKIAEKLKISPAAVTKALKLQEQLIKSSRATNDERRVVLWSLTEKAV 101
 Sbjct 40 IAMLAIENKMTINKLGEELSLSGTLSPLLRKLEAKGYIVRKRSQDKERSVELFLTDKGA 99

Query 102 PVAKE 106
 Sbjct 100 QVKKE 104

>ref|YP_001031675.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
 Length=157

GENE ID: 4798013 napB | MarR family transcriptional regulator
 [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 35.4 bits (80), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 23/83 (27%), Positives = 45/83 (54%), Gaps = 0/83 (0%)

Query 55 KIAEKLKISPAAVTKALKLQEQLIKSSRATNDERRVVLWSLTEKAVPVAKEHATHHEKT 114
 Sbjct 58 KLAHHLYMTRGAASKIAKKLLKKNLIESYQIPQNKKEIYFRLTKEGQQINDRHESLHQKF 117

Query 115 LSTYQELGNKFTDEEQEVISKFL 137
 Sbjct 118 SQNDQVIFDELTDSEVSNILEFL 140

>ref|NP_266898.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. lactis I11403]
 Length=158

GENE ID: 1114368 rmaA | MarR family transcriptional regulator
 [Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 35.4 bits (80), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 22/66 (33%), Positives = 36/66 (54%), Gaps = 3/66 (4%)

Query 41 HILMLLAEQISTNA---KIAEKLKISPAAVTKALKLQEQLIKSSRATNDERRVVLWSLT 97
 Sbjct 42 QLLCLISLYIKDNQSSEQITDDLSIDKSSVHRAIKGLIEKEYVSRVRDEKDKRVYRVSLT 101

Query 98 EKAVPV 103
 Sbjct 102 QKARDI 107

>ref|YP_808372.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
 Length=157

GENE ID: 4434175 LACR_0343 | MarR family transcriptional regulator
 [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 35.4 bits (80), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 23/83 (27%), Positives = 45/83 (54%), Gaps = 0/83 (0%)

Query 55 KIAEKLKISPAAVTKALKLQEQLIKSSRATNDERRVVLWSLTEKAVPVAKEHATHHEKT 114
 Sbjct 58 KLAHHLYMTRGAASKIAKKLLKKNLIESYQIPQNKKEIYFRLTKEGQQINDRHESLHQKF 117

Query 115 LSTYQELGNKFTDEEQEVISKFL 137
 Sbjct 118 SQNDQVIFDELTDSEVSNILEFL 140

>ref|YP_001031774.1| **G** transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
 Length=166

Annex 2

GENE ID: 4798362 llmg_0424 | transcriptional regulator
 [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 35.0 bits (79), Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 29/111 (26%), Positives = 53/111 (47%), Gaps = 13/111 (11%)

Query 39	QEHIIMLLAEQISTNAKIAEK----LKISPAAVTKALKKLQEQEELIKSSRATNDERVVL	93
	Q IL +L E N+K+ +K L + P + ++ +KKL+++ I + D+R + SLT	
Sbjct 43	QGQILNLME---NSKMTQKNLVAQLDMRPQSASEMIKKLEKKQFISRQKDAQDKRGFI	98
Query 94	WSLTEKAVPVAKHEATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF	144
	SLTEK V +E + + FT+EE+ ++ + L E	
Sbjct 99	ISLTEKGKAVLEESTEQTGRVPG---IMTSFTEEKIEFARLIGKLQSEL	145

>ref|YP_001031879.1| **G** putative transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
 Length=156

GENE ID: 4796958 llmg_0529 | putative transcriptional regulator
 [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 32.3 bits (72), Expect = 0.017, Method: Compositional matrix adjust.
 Identities = 18/62 (29%), Positives = 38/62 (61%), Gaps = 7/62 (11%)

Query 33	VKLSTSQE---HILMLLAE---QISTNAKIAEKLKISPAAVTKALKKLQEQEELIKSSRA	85
	+KL+S E ++L++LA + ++ +A +LK+SP+ + K +K L ++ L++S+	
Sbjct 1	MKLSSGWEQSVYVLLILARLPENRTMSSIALANRLKVSPSYLKKIIKSLVDEGLLRSTTG	60
Query 86	TN 87	
	N	
Sbjct 61	KN 62	

>ref|YP_808573.1| **G** BadM/Rrf2 family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
 Length=156

GENE ID: 4433945 LACR_0579 | BadM/Rrf2 family transcriptional regulator
 [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 32.3 bits (72), Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 18/62 (29%), Positives = 38/62 (61%), Gaps = 7/62 (11%)

Query 33	VKLSTSQE---HILMLLAE---QISTNAKIAEKLKISPAAVTKALKKLQEQEELIKSSRA	85
	+KL+S E ++L++LA + ++ +A +LK+SP+ + K +K L ++ L++S+	
Sbjct 1	MKLSSGWEQSVYVLLILARLPENRTMSSIALANRLKVSPSYLKKIIKSLVDEGLLRSTTG	60
Query 86	TN 87	
	N	
Sbjct 61	KN 62	

>ref|NP_266714.1| **G** hypothetical protein L153086 [Lactococcus lactis subsp. lactis I11403]
 Length=156

GENE ID: 1114177 yffB | hypothetical protein
 [Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 32.3 bits (72), Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 18/62 (29%), Positives = 38/62 (61%), Gaps = 7/62 (11%)

Query 33	VKLSTSQE---HILMLLAE---QISTNAKIAEKLKISPAAVTKALKKLQEQEELIKSSRA	85
	+KL+S E ++L++LA + ++ +A +LK+SP+ + K +K L ++ L++S+	
Sbjct 1	MKLSSGWEQSVYVLLILARLPENRTMSSIALANRLKVSPSYLKKIIKSLVDEGLLRSTPG	60
Query 86	TN 87	
	N	
Sbjct 61	KN 62	

>ref|YP_001033090.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
 Length=160

GENE ID: 4798315 rmaA | MarR family transcriptional regulator
 [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 31.6 bits (70), Expect = 0.031, Method: Compositional matrix adjust.
 Identities = 29/107 (27%), Positives = 52/107 (48%), Gaps = 10/107 (9%)

Query 41	HILMLLAEIQISTNA---KIAEKLKISPAAVTKALKKLQEQEELIKSSRATNDERVVLWSLT	97
	+L L++ I N +I + L I +V +A++ L E+E + R +D+R SLT	
Sbjct 42	QLLCLISLYIKDNQSQEQITDDLSIDKSSVHRAIRSLIEKEYVVRVRDEHDKRAYRVSLT	101
Query 98	EKAVPVAK--EHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTE	142
	+KA + E T + L L +E+E+ K L+ +T+	

Sbjct 102 KKARAIQSQIEEMTKERENL----LSEGIDPKEKEIAFKVLNQMTQ 143

>ref|YP_808765.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=155

GENE ID: 4432345 LACR_0786 | MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 31.6 bits (70), Expect = 0.034, Method: Compositional matrix adjust.
Identities = 20/65 (30%), Positives = 36/65 (55%), Gaps = 3/65 (4%)

Query 42 IMLLAAEQISTNA---KIAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWSLTE 98
+L L++ I N +I + L I ++V +A++ L E+E + R +D+R SLT+
Sbjct 43 LLCLISLYIKDNQSQEQTDDLSIDKSSVHRAIRSLIEKEYVVVRVDRDEHDKRAYRVSLTK 102

Query 99 KAVPV 103
KA +
Sbjct 103 KARAI 107

>ref|YP_808795.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]

ref|YP_001033061.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=146

GENE ID: 4433123 LACR_0820 | MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 31.2 bits (69), Expect = 0.044, Method: Compositional matrix adjust.
Identities = 19/57 (33%), Positives = 31/57 (54%), Gaps = 3/57 (5%)

Query 56 IAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWSLTEKAVPVAKEHATHHE 112
IA+ K++ + +T L +L+++ I+ R+T D RV LT K + ATH E
Sbjct 57 IAKNQKLALSTITITLNRLLEDKGYIERKRSTADRRVTIIILTSKGDEL---ATHRE 110

>ref|NP_266926.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. lactis II1403]
Length=146

GENE ID: 1114397 rmaG | MarR family transcriptional regulator [Lactococcus lactis subsp. lactis II1403] (10 or fewer PubMed links)

Score = 31.2 bits (69), Expect = 0.045, Method: Compositional matrix adjust.
Identities = 19/57 (33%), Positives = 31/57 (54%), Gaps = 3/57 (5%)

Query 56 IAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWSLTEKAVPVAKEHATHHE 112
IA+ K++ + +T L +L+++ I+ R+T D RV LT K + ATH E
Sbjct 57 IAKNQKLALSTITITLNRLLEDKGYIERKRSTADRRVTIIILTSKGDEL---ATHRE 110

>ref|YP_001032909.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=154

GENE ID: 4797429 rmaH | MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 28.9 bits (63), Expect = 0.18, Method: Compositional matrix adjust.
Identities = 24/85 (28%), Positives = 41/85 (48%), Gaps = 1/85 (1%)

Query 54 AKIAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEK 113
+KIA+ S A + L L+ + LI + D R +L ++T+K VA+E
Sbjct 51 SKIAKFHTSTARIAITILNNLESKNLITREISRTDRRKILVAITDKGRRVAEEIRVEACS 110

Query 114 TLS-TYQELGNKFTDEEQEVISKFL 137
L+ ++E+G + T+ E FL
Sbjct 111 NLARVFKEMGERTESFIENFKMFL 135

>ref|YP_001032520.1| **G** MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=127

GENE ID: 4797914 rmaX | MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 28.1 bits (61), Expect = 0.31, Method: Compositional matrix adjust.
Identities = 24/86 (27%), Positives = 36/86 (41%), Gaps = 6/86 (6%)

Query 54 AKIAEKLKISPAAVTKALKLQEQLIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEK 113
+ IA + S A V L L+E+ +I + D R +L LT+K KE T
Sbjct 29 SDIARYIGASTARVANILNNLEEKGMISREISREDRRRKILVFLTDKGRKETKERRTR--- 85

Query 114 TLSTYQELGNKFTDEEQEVISKFLSA 139
 T + N F +E +F+ A
 Sbjct 86 ---TITRISNVFEAMGEERTQQFIEA 108

>ref|NP_267064.1| **G** transcription regulator [Lactococcus lactis subsp. lactis Ill1403]
 Length=154

GENE ID: 1114538 rmaH | transcription regulator
 [Lactococcus lactis subsp. lactis Ill1403] (10 or fewer PubMed links)

Score = 28.1 bits (61), Expect = 0.35, Method: Compositional matrix adjust.
 Identities = 23/85 (27%), Positives = 41/85 (48%), Gaps = 1/85 (1%)

Query 54 AKIAEKLKISPAAVTKALKLQEQUELIKSSRATNDERVVVLWSLTEKAVPVAKEHATHHEK 113
 +KIA+ S A + L L+ + L+ + D R +L ++T+K VA+E
 Sbjct 51 SKIAKFHTSTARIAТИЛННLESKNLVTRЕISRTDRRKILVAITDKGRHVAAЕIRVEACS 110

Query 114 TLS-TYQELGNKFTDEEQEVISKFL 137
 L+ ++E+G + T+ E FL
 Sbjct 111 NLARVFEEМGEERTESFIENFKLFL 135

>ref|YP_001032533.1| **G** transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
 Length=217

GENE ID: 4798916 llmg_1224 | transcriptional regulator
 [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 28.1 bits (61), Expect = 0.38, Method: Compositional matrix adjust.
 Identities = 14/33 (42%), Positives = 24/33 (72%), Gaps = 1/33 (3%)

Query 48 EQISTNAKIAEKLKISPAAVTKALKLQEQUELI 80
 E +S NA IA+KL +S + T+ +K+L ++EL+
 Sbjct 23 ESVSINA-IAQKLSVSSPSATEMIKRLAKKELV 54

>ref|YP_809312.1| **G** Mn-dependent transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
 Length=217

GENE ID: 4432558 LACR_1369 | Mn-dependent transcriptional regulator
 [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 28.1 bits (61), Expect = 0.38, Method: Compositional matrix adjust.
 Identities = 14/33 (42%), Positives = 24/33 (72%), Gaps = 1/33 (3%)

Query 48 EQISTNAKIAEKLKISPAAVTKALKLQEQUELI 80
 E +S NA IA+KL +S + T+ +K+L ++EL+
 Sbjct 23 ESVSINA-IAQKLSVSSPSATEMIKRLAKKELV 54

>ref|NP_267461.1| **G** transcription regulator [Lactococcus lactis subsp. lactis Ill1403]
 Length=156

GENE ID: 1114954 rmaF | transcription regulator
 [Lactococcus lactis subsp. lactis Ill1403] (10 or fewer PubMed links)

Score = 27.7 bits (60), Expect = 0.42, Method: Compositional matrix adjust.
 Identities = 15/45 (33%), Positives = 24/45 (53%), Gaps = 0/45 (0%)

Query 56 IAEKLKISPAAVTKALKLQEQUELIKSSRATNDERVVVLWSLTEKA 100
 + E L IS A+ + L+E+EL+ ND+R+ LTE+
 Sbjct 63 LLEVLDISKQALNGPMNDLKEKELVHFKPNNENDKRIKQLYLTEQG 107

>ref|NP_267696.1| **G** transcription regulator [Lactococcus lactis subsp. lactis Ill1403]
 Length=148

GENE ID: 1115197 rmaI | transcription regulator
 [Lactococcus lactis subsp. lactis Ill1403] (10 or fewer PubMed links)

Score = 27.3 bits (59), Expect = 0.61, Method: Compositional matrix adjust.
 Identities = 32/142 (22%), Positives = 60/142 (42%), Gaps = 18/142 (12%)

Query 11 LGTIMQFAENKHEILLGKCESDVKLTSTQEHIMLLAEQISTNAK-----IAEKLKIS 63
 +G +++ A N+ + + LT Q IL L Q ++ I + I
 Sbjct 8 IGRLLKVASNQMSREFDNFAAQLDLTGQQMSILDFLGNQSEEDSGKEISQTMIELEFNIR 67

Query 64 PAAVTKALKLQEQUELIKSSRATNDERVVVLWSLTEKAVPVAKEHAT---HHEKTLSTYQ 119
 + T+ L++++++LIK + D R LTE+ E T H++K L+
 Sbjct 68 RSTTTEILQRMEKRQLIKRKASPTDARQSVELTEEGKQYLPEIRTYIQGHNQKALAG-- 125

Query 120 ELGNKFTDEEQEVISKFLSALT 141
 + EE + KFL+ +
 Sbjct 126 -----LSAEEIAAVEKFLNNFS 142

>ref|NP_266753.1| **G** NADPH-flavin oxidoreductase [Lactococcus lactis subsp. lactis I11403]
Length=216

GENE ID: 1114217 yfiJ | NADPH-flavin oxidoreductase
 [Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

 Score = 27.3 bits (59), Expect = 0.67, Method: Compositional matrix adjust.
 Identities = 11/29 (37%), Positives = 18/29 (62%), Gaps = 0/29 (0%)

 Query 109 THHEKTLSTYQELGNKFTDEEQEVISKFL 137
 +HH+K+ QE+ N T +E ++KFL
 Sbjct 180 SHHQKSTDWTQEMSNFLTKPRREDVAKFL 208

>ref|NP_267412.1| **G** metalloregulator [Lactococcus lactis subsp. lactis I11403]
Length=217

GENE ID: 1114905 ymiA | metalloregulator
 [Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

 Score = 26.6 bits (57), Expect = 1.1, Method: Compositional matrix adjust.
 Identities = 13/31 (41%), Positives = 23/31 (74%), Gaps = 1/31 (3%)

 Query 50 ISTNAKIAEKLKISPAAVTKALKLQEQUELI 80
 +S NA IA+KL +S + T+ +K+L ++EL+
 Sbjct 25 VSINA-IAQKLSVSSPSATEMIKRLAKKELV 54

>ref|YP_001031697.1| **G** putative cobalt ABC transporter ATP-binding protein [Lactococcus lactis subsp. cremoris MG1363]
Length=565

GENE ID: 4798558 cbio | putative cobalt ABC transporter ATP-binding protein
 [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

 Score = 26.2 bits (56), Expect = 1.2, Method: Compositional matrix adjust.
 Identities = 12/27 (44%), Positives = 17/27 (62%), Gaps = 0/27 (0%)

 Query 55 KIAEKLKISPAAVTKALKLQEQUELIK 81
 ++A K ISP ++TKA Q QE +K
 Sbjct 537 QLARKADISPISLTKAFAINFQNQERLK 563

>ref|NP_266873.1| **G** quinone oxidoreductase [Lactococcus lactis subsp. lactis I11403]
Length=328

GENE ID: 1114342 qor | quinone oxidoreductase
 [Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

 Score = 25.4 bits (54), Expect = 2.4, Method: Compositional matrix adjust.
 Identities = 10/19 (52%), Positives = 11/19 (57%), Gaps = 0/19 (0%)

 Query 109 THHEKTLSTYQELGNKFTD 127
 HHEK + ELG KF D
 Sbjct 193 NHHEKLVPQVHELGFKFVD 211

>ref|NP_268402.1| **G** alkylphosphonate uptake protein [Lactococcus lactis subsp. lactis I11403]
Length=114

GENE ID: 1115923 phnA | alkylphosphonate uptake protein
 [Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

 Score = 25.4 bits (54), Expect = 2.4, Method: Compositional matrix adjust.
 Identities = 14/41 (34%), Positives = 19/41 (46%), Gaps = 0/41 (0%)

 Query 97 TEKAVPVAAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFL 137
 T K + + E+ T E GN+FT EE E KF+
 Sbjct 3 TPKCIHCSSEYYTYESDTSFGCSECGNEFTLEEIEAAGKFI 43

>ref|YP_808209.1| **G** transcriptional repressor CodY [Lactococcus lactis subsp. cremoris SK11]
Length=262

GENE ID: 4434653 LACR_0168 | transcriptional repressor CodY
 [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

 Score = 24.6 bits (52), Expect = 3.4, Method: Compositional matrix adjust.
 Identities = 10/27 (37%), Positives = 19/27 (70%), Gaps = 0/27 (0%)

 Query 56 IAEKLKISPAAVTKALKLQEQUELIKS 82
 IA+K+ I+ + + AL+KL+ +I+S

Sbjct 210 IADKIGITRSVIVNALKLESAGVIES 236

>ref|YP_001031533.1| **G** transcriptional repressor CodY [Lactococcus lactis subsp. cremoris MG1363]
Length=262

GENE ID: 4797198 codY | transcriptional repressor CodY [Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 3.4, Method: Compositional matrix adjust.
Identities = 10/27 (37%), Positives = 19/27 (70%), Gaps = 0/27 (0%)

Query 56 IAEKLKISPAAVTKALKKLQEQQELIKS 82

IA+K+ I+ + + AL+KL+ +I+S

Sbjct 210 IADKIGITRSVIVNALKLESAGVIES 236

>ref|NP_266317.1| **G** transcriptional repressor CodY [Lactococcus lactis subsp. lactis Il1403]
Length=262

GENE ID: 1113769 codY | transcriptional repressor CodY [Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 3.5, Method: Compositional matrix adjust.
Identities = 10/27 (37%), Positives = 19/27 (70%), Gaps = 0/27 (0%)

Query 56 IAEKLKISPAAVTKALKKLQEQQELIKS 82

IA+K+ I+ + + AL+KL+ +I+S

Sbjct 210 IADKIGITRSVIVNALKLESAGVIES 236

>ref|NP_266838.1| **G** intercellular adhesion protein [Lactococcus lactis subsp. lactis Il1403]
Length=276

GENE ID: 1114306 icaB | intercellular adhesion protein [Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 3.6, Method: Compositional matrix adjust.
Identities = 14/46 (30%), Positives = 21/46 (45%), Gaps = 0/46 (0%)

Query 43 LMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQQELIKSSRATND 88

L L Q K+ + + S + K +KK+ E L+ S TND

Sbjct 126 LDLPFTQFIITGKVGTIDGSQMSTWKEIKMMNENPLVTSGLHTND 171

>ref|NP_266710.1| **G** transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=247

GENE ID: 1114173 yfeA | transcription regulator [Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 3.6, Method: Compositional matrix adjust.
Identities = 16/44 (36%), Positives = 25/44 (56%), Gaps = 5/44 (11%)

Query 35 LTSTQEHHILMLLAEQIS----TNAKIAEKLKISPAAVTKALKK 73

LTS + + I L E + T A+IAE +SP+++ + LKK

Sbjct 4 LTSVEIYIWNYLEENKAKIIQMTVAQIAESAHVSPSSIIRTLKK 47

>ref|NP_266438.1| **G** amino acid amidohydrolase [Lactococcus lactis subsp. lactis Il1403]
Length=384

GENE ID: 1113892 yciA | amino acid amidohydrolase [Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 4.1, Method: Compositional matrix adjust.
Identities = 11/41 (26%), Positives = 17/41 (41%), Gaps = 7/41 (17%)

Query 8 DQFLGT-----IMQFAENKHEILLGKCESDVKLTSTQEH 41

D+F G + A N+H + G CE ++ T H

Sbjct 147 DEFYGLHVRPDLKVGDIATNQHTLFAGTCVELSFIGTGGH 187

>ref|YP_808446.1| **G** lysyl-tRNA synthetase [Lactococcus lactis subsp. cremoris SK11]
Length=794

GENE ID: 4433352 lysS | lysyl-tRNA synthetase [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 24.6 bits (52), Expect = 4.3, Method: Composition-based stats.
Identities = 12/34 (35%), Positives = 20/34 (58%), Gaps = 0/34 (0%)

Query 98 EKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQE 131
E+A +AKEH H EK ++ + N+F ++ E

Sbjct 340 EEATALAKEHDIHVEKHFTSVGHIINEFFEKYVE 373

>ref|YP_001031741.1| **G** lysyl-tRNA synthetase [Lactococcus lactis subsp. cremoris MG1363]
Length=794

GENE ID: 4799123 lysS | lysyl-tRNA synthetase
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 24.3 bits (51), Expect = 4.7, Method: Composition-based stats.
Identities = 12/34 (35%), Positives = 20/34 (58%), Gaps = 0/34 (0%)

Query 98 EKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQE 131
E+A +AKEH H EK ++ + N+F ++ E
Sbjct 340 EEATALAKEHDIHVEKHFTSVGHIINEFFEKYVE 373

>ref|NP_266529.1| **G** lysyl-tRNA synthetase [Lactococcus lactis subsp. lactis Il1403]
Length=794

GENE ID: 1113984 lysS | lysyl-tRNA synthetase
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 24.3 bits (51), Expect = 4.7, Method: Composition-based stats.
Identities = 12/34 (35%), Positives = 20/34 (58%), Gaps = 0/34 (0%)

Query 98 EKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQE 131
E+A +AKEH H EK ++ + N+F ++ E
Sbjct 340 EEATALAKEHDIHVEKHFTSVGHIINEFFEKYVE 373

>ref|YP_001031907.1| **G** NADPH-flavin oxidoreductase [Lactococcus lactis subsp. cremoris MG1363]
Length=251

GENE ID: 4798593 llmg_0559 | NADPH-flavin oxidoreductase
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 24.3 bits (51), Expect = 5.2, Method: Compositional matrix adjust.
Identities = 9/29 (31%), Positives = 19/29 (65%), Gaps = 0/29 (0%)

Query 109 THHEKTLSTYQELGNKFTDEEQEVISKFL 137
+HH+K+ + QE+ + T+ +E ++ FL
Sbjct 215 SHHQKSTNWSQEMSDFLTNPRREDLDFL 243

>ref|YP_808603.1| **G** NADPH-flavin oxidoreductase [Lactococcus lactis subsp. cremoris SK11]
Length=251

GENE ID: 4433732 LACR_0613 | NADPH-flavin oxidoreductase
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 24.3 bits (51), Expect = 5.5, Method: Compositional matrix adjust.
Identities = 9/29 (31%), Positives = 19/29 (65%), Gaps = 0/29 (0%)

Query 109 THHEKTLSTYQELGNKFTDEEQEVISKFL 137
+HH+K+ + QE+ + T+ +E ++ FL
Sbjct 215 SHHQKSTNWSQEMSDFLTNPRREDLADFL 243

>ref|NP_268293.1| **G** exported serine protease [Lactococcus lactis subsp. lactis Il1403]
Length=408

GENE ID: 1115813 htrA | exported serine protease
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 23.9 bits (50), Expect = 6.1, Method: Compositional matrix adjust.
Identities = 17/59 (28%), Positives = 34/59 (57%), Gaps = 5/59 (8%)

Query 15 MQFAENKHEI--LLGKCESDVKLSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKAL 71
+ FA +++ ++ K E+D K++ I M+ Q+STN + +LK+ P++VT +
Sbjct 271 LGFAIPSNDVNIINKLEADGKISRPALEGIRMVVDLSQLSTND--SSQLKL-PSSVTGGV 326

>ref|YP_001033660.1| **G** housekeeping protease [Lactococcus lactis subsp. cremoris MG1363]
Length=407

GENE ID: 4797497 htrA | housekeeping protease
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 23.9 bits (50), Expect = 6.5, Method: Compositional matrix adjust.
Identities = 17/59 (28%), Positives = 34/59 (57%), Gaps = 5/59 (8%)

Query 15 MQFAENKHEI--LLGKCESDVKLSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKAL 71
+ FA +++ ++ K E+D K++ I M+ Q+STN + +LK+ P++VT +
Sbjct 270 LGFAIPSNDVNIINKLETDGKISRPALEGIRMVVDLSQLSTND--SSQLKL-PSSVTGGV 325

Annex 2

>ref|YP_811995.1| **G** trypsin-like serine protease [Lactococcus lactis subsp. cremoris SK11]
Length=407

GENE ID: 4432303 LACR_2439 | trypsin-like serine protease
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 23.9 bits (50), Expect = 6.6, Method: Compositional matrix adjust.
Identities = 17/59 (28%), Positives = 34/59 (57%), Gaps = 5/59 (8%)

Query 15 MQFAENKHEI--LLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKAL 71
+ FA +++ ++ K E+D K++ I M+ Q+STN + +LK+ P++VT +
Sbjct 270 LGFAIPSNDVVIINKLETDGKISRPALEGIRMVDSLSQLSTND--SSQLKL-PSSVTGGV 325

>ref|NP_268332.1| **G** hypothetical protein L35545 [Lactococcus lactis subsp. lactis I11403]

ref|YP_812032.1| **G** hypothetical protein LACR_2483 [Lactococcus lactis subsp. cremoris SK11]

ref|YP_001033699.1| **G** hypothetical protein l1mg_2459 [Lactococcus lactis subsp. cremoris MG1363]
Length=82

GENE ID: 1115852 ywfB | hypothetical protein
[Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 7.5, Method: Compositional matrix adjust.
Identities = 13/29 (44%), Positives = 14/29 (48%), Gaps = 0/29 (0%)

Query 97 TEKAVPVAKEHATHHEKTLSYQELGNKF 125
TE AKE A +E L YQ L KF
Sbjct 34 TEDGKKEAKEAAIRYESRLDAYQFLQGKF 62

>ref|NP_268337.1| **G** hypothetical protein L39650 [Lactococcus lactis subsp. lactis I11403]
Length=926

GENE ID: 1115857 ywfG | hypothetical protein
[Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 7.7, Method: Composition-based stats.
Identities = 11/25 (44%), Positives = 13/25 (52%), Gaps = 0/25 (0%)

Query 118 YQELGNKFTDEEQEVISKFLSALTE 142
Y E G KF D+ Q I + LTE
Sbjct 557 YPEDGTFADDPQHYIVRLKHGLTE 581

>ref|YP_001032772.1| **G** superfamily II DNA/RNA helicase [Lactococcus lactis subsp. cremoris MG1363]
Length=430

GENE ID: 4797767 comFA | superfamily II DNA/RNA helicase
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 7.8, Method: Compositional matrix adjust.
Identities = 17/46 (36%), Positives = 26/46 (56%), Gaps = 1/46 (2%)

Query 34 KLTSTQEHIMLLAEQISTNAKIAEKLKISPAAVTKALKLQEQEL 79
KLT QE I L +QI+ N K+ + ++ A T+ + +L EQ L
Sbjct 105 KLLENQEKSNALCQQITNNQKLLVQ-AVTGAGKTEMIYQLEQIL 149

>ref|YP_001033122.1| **G** quinone oxidoreductase [Lactococcus lactis subsp. cremoris MG1363]
Length=328

GENE ID: 4798878 qor | quinone oxidoreductase
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 9.3, Method: Compositional matrix adjust.
Identities = 9/18 (50%), Positives = 10/18 (55%), Gaps = 0/18 (0%)

Query 110 HHEKTLSTYQELGNKFTD 127
HHE + ELG KF D
Sbjct 194 HHENLVPQVHELGFKFVD 211

>ref|YP_808733.1| **G** quinone oxidoreductase [Lactococcus lactis subsp. cremoris SK11]
Length=328

GENE ID: 4432226 LACR_0751 | quinone oxidoreductase
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Annex 2

Score = 23.5 bits (49), Expect = 9.3, Method: Compositional matrix adjust.
 Identities = 9/18 (50%), Positives = 10/18 (55%), Gaps = 0/18 (0%)

Query 110 HHEKTLSTYQELGNKFTD 127
 HHE + ELG KF D
 Sbjct 194 HHENLVPQVHELGKFVVD 211

>ref|YP_796521.1| **G** hypothetical protein LACR_C57 [Lactococcus lactis subsp. cremoris SK11]
 Length=330

GENE ID: 4405852 LACR_C57 | hypothetical protein
 [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 9.5, Method: Compositional matrix adjust.
 Identities = 11/33 (33%), Positives = 22/33 (66%), Gaps = 0/33 (0%)

Query 53 NAKIAEKLKISPAAVTKALKKLQEQLIKSSRA 85
 N K ++L S + ++A K+Q Q+L+K+S++
 Sbjct 189 NIKDTQELDFSSSNFSEAQLKVQNQDLVKNSKS 221

>ref|YP_812095.1| **G** hypothetical protein LACR_2554 [Lactococcus lactis subsp. cremoris SK11]
 Length=114

GENE ID: 4432134 LACR_2554 | hypothetical protein
 [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 23.1 bits (48), Expect = 10.0, Method: Compositional matrix adjust.
 Identities = 13/41 (31%), Positives = 18/41 (43%), Gaps = 0/41 (0%)

Query 97 TEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFL 137
 T K + + E+ E GN+FT EE E KF+
 Sbjct 3 TPKCIHCSSEYTYELSDMSFGCSECNEFTLEEIEAAGKFI 43

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